

GenCore version 5.1.8
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OM protein - nucleic search, using frame_plus.p2n model

Run on: May 22, 2006, 22:22:11 ; Search time 50 Seconds
(without alignments)
1602.325 Million cell updates/sec

Title: US-09-419-679-6
Sequence: 1 MWKLFARAGGNFWLRTLNHH.....KNIPFWALGEYQSVQLQSR 757

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 448628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-TRANSHUMAN=0.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: Published Applications NA.New:
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8: /EMC_Celerra_SIDS3/prodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	736	17.7	1440	US-11-217-529-5566	Sequence 5566, Ap
2	482.5	11.6	642	US-11-217-529-5565	Sequence 5565, Ap
3	470.5	11.3	696	US-11-217-529-173919	Sequence 173919, Ap
4	412	9.9	750	US-11-217-529-174234	Sequence 174234, Ap
5	195.5	4.7	516	US-11-217-529-166803	Sequence 166803, Ap
6	100.5	2.4	5778	US-11-217-529-5615	Sequence 5615, Ap
7	98.5	2.4	2466	US-11-217-529-5352	Sequence 5352, Ap
8	98	2.4	2037	US-11-217-529-80385	Sequence 80385, Ap
9	97	2.3	1743	US-11-145-307A-42	Sequence 42, Appl

10	97	2.3	4179	US-11-217-529-75536	Sequence 75536, A
11	96	2.3	1692	US-11-217-529-551	Sequence 551, App
12	96	2.3	6928	US-10-505-928-781	Sequence 781, App
13	94.5	2.3	2586	US-11-217-529-3854	Sequence 3854, Ap
14	94.5	2.3	3951	US-10-196-749-119	Sequence 119, App
15	94	2.3	128361	US-10-505-928-151	Sequence 151, App
16	93.5	2.3	2872	US-11-145-307A-3	Sequence 3, Appl
17	93.5	2.3	8448	US-11-145-307A-166	Sequence 166, App
18	93.5	2.2	2331	US-10-196-749-59	Sequence 59, Appl
19	92.5	2.2	978	US-11-217-529-2736	Sequence 2736, Ap
20	91	2.2	1437	US-11-217-529-79716	Sequence 79716, A
21	91	2.2	2130	US-11-217-529-173-52	Sequence 2017, Ap
22	91	2.2	8178	US-10-473-173-52	Sequence 52, Appl
23	90.5	2.2	151830	US-10-519-335-37	Sequence 37, Appl
24	89.5	2.2	1431	US-11-242-505A-11	Sequence 10, Appl
25	89.5	2.2	1821	US-11-242-505A-10	Sequence 5543, Ap
26	88.5	2.1	2001	US-11-217-529-5543	Sequence 75343, A
27	88	2.1	2142	US-11-217-529-75343	Sequence 4068, Ap
28	88	2.1	4209	US-11-217-529-4068	Sequence 129, App
29	88	2.1	10448	US-11-024-544A-129	Sequence 112, App
30	88	2.1	10448	US-11-190-750-112	Sequence 123, App
31	88	2.1	10448	US-11-264-784-123	Sequence 125, App
32	88	2.1	13295	US-11-264-784-125	Sequence 127, App
33	88	2.1	15543	US-11-264-784-124	Sequence 4397, Ap
34	88	2.1	16325	US-11-264-784-127	Sequence 3997, App
35	87.5	2.1	2307	US-11-217-529-4497	Sequence 77675, A
36	87.5	2.1	3475	US-10-511-937-399	Sequence 27, Appl
37	87	2.1	2475	US-11-217-529-77675	Sequence 76818, A
38	87	2.1	4168	US-11-106-014-27	Sequence 81170, A
39	86.5	2.1	1444	US-11-217-529-76818	Sequence 1657, Ap
40	86.5	2.1	4143	US-11-217-529-81170	Sequence 1, Appl
41	86.5	2.1	4611	US-11-217-529-191207	Sequence 3180, Ap
42	86	2.1	2136	US-11-217-529-1657	Sequence 1482, Ap
43	86	2.1	3743	US-10-502-993-1	
44	85.5	2.1	1071	US-11-217-529-3180	
45	85.5	2.1	3147	US-11-217-529-1482	

ALIGNMENTS

RESULT 1
US-11-217-529-5566
Sequence 5566, Application US/11217529
Publication No. US2006009612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217, 529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5566
LENGTH: 1440
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-5566

Alignment Scores:
Pred. No.: 4.16e-65
Score: 736.00
Percent Similarity: 49.7%
Best Local Similarity: 37.8%
Query Match: 17.7%
Length: 1440
Matches: 191
Conservative: 60
Mismatch: 188
Indels: 66
Gaps: 17

10/607726

US-09-419-679-6 (1-757) x US-11-217-529-5565 (1-1440)

QY 2 TrrpYvleuYvRphAlaGluGlyLeuAnProtrPleuArgThrLeuAsnHisVal 21
|||
Db 55 TGGAGATTAAAGATCGATGAAATCA----- 78

QY 22 GluArgGlnValTrrpGluRheArProYvleuGlySerProGlnAerPleuGluLe 41
|||
Db 79 GCGCGAAGAAAGCTGGGAATAC-----TTGACGCT 108

QY 42 GluYvAlaArgGlnAerPheHisvArPheArPheThrHisvLeuHisSerAlaerPleu 61
|||
Db 109 GAGCAAGCA---GCTAAAGCAAGCCGCCATCTTCAACAATGAG-----CTT 153

QY 62 LeuMetArgMetGlnRheAlaArgGluAnProThrArgGlnValLeuProYvAlaGly 81
|||
Db 154 CTTCAGATCCAGACTTCTCAACCCACCGAAGAAAGAAC----- 195

QY 82 ValYvArPrlleGluArPvalThrGlnGluLeValThrYvThrLeuArgAlaVal 101
|||
Db 196 ---AAGCATTCACAGACTTTTGC-----GCTTCGATGCTGCCATTAAGCGTGA 243

QY 102 SerPheHisSerThrLeuGlnCyvHisvAr---GluHisTrpProGlyArPTrGlyGly 120
|||
Db 244 TCTTCTTCAAACTCTGCAAGAGCCCGATTCGGTATTTTCCATGCAATATTAAGGG 303

QY 121 PrometRheLeuMetProGlyLeuValIleThrLeuSerIleThrGlyAlaLeuAsnThr 140
|||
Db 304 CCGATGTTCAATGACAAATGGTATATGCTGTGAGCTATATTTGCTGGC-----ATT 354

QY 141 ValLeuThrGlnGluHisvArgYvGluLeCyvArGlyTrLeuYvArHisvGlnAnYv 160
|||
Db 355 CAATTCCTGAAACATGAAGATAGATTAATCAATCATCTGTAACAACGCGACATCCC 414

QY 161 ---AerGlyGlyTrpGlyLeuHisvIleGluGlyProSerThrMetPheGlySerValLeu 179
|||
Db 415 GTCCATGCTGGTGGGGGTGGCATCCCGTGCAAAATCTAGCTTTTGGTATCTACTG 474

QY 180 SerYvIleThrLeuArgLeuLeuGlyGluGlyProAnArPerglyGlnGlyMetCly 199
|||
Db 475 AACTATGTTATTTTGGCTGTGTAGCGCTATCGAAGAAAT-----CATCCGTTTGTGTC 528

QY 200 LysAlaArgArPTrIleLeuGlyHisvGlyGlyAlaThrYvIleThrSerTrpGlyYv 219
|||
Db 529 AAGGCAAGAGATCTTTATTAAGATTAAGCGGTGCTATCGGGCCCACTGGGGCAAA 588

QY 220 MetTrpLeuSerValLeuGlyValYvGluTrpSerGlyYvAnArPleuProGlu 239
|||
Db 589 GTTGGCTAAGTGCATTAACCTGTATTAATGGAAAGGTGTTAACCTGCTCTCTGAA 648

QY 240 IleTrpLeuLeuProTrpMetLeuProPheHisvProGlyYvArMetTrpCyvHisvArg 259
|||
Db 649 ACTGGCTACTTCGGTACTCATCTGCTATTCATCCAGAAAGATGGTGGGTTCAATAGA 708

QY 260 MetValYvLeuProMetSerYvLeuYvGlyYvArPheValGlyProIleSerPro 279
|||
Db 709 GCGCTTACATTCACGTCAGTAACTGTCATTTGTAAGAGTTGTAAGTCCATGACTCT 768

QY 280 ThrValLeuSerLeuArgYvGlyLeuYvTrpThrValProYvHisvArPrlleArPTrArP 299
|||
Db 769 CTTCCTTGAAGATTAAGGGGTGAATTTAAGCTCAAAACATTTGATTAAGATTAACCTTTCT 828

QY 300 GlnAlaArgAnPleuCyvAlaYvGlyArPleuYvTrpProHisvProLeuValGlnArP 319
|||
Db 829 AACCAAGAAACACTGTGTGTGGAGTGAATTTATTTATTCACACTTAAATTTTGAT 888

QY 320 IleLeuTrpAlaSerLeuHisvArPheLeuGluProIleLeuMetHisvTrpProGlyYv 339
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Db 889 ATTGCAAAATGTTTGTG---GTATTTAAGAA-----AAA 921

QY 340 ArgLeuArgGlyYvAlaIleIleSer-----AlaLeuGlnHisvIleHis 354
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Db 922 TACTTGAAAGATTCATTTATTTCTTATTCAGAGAAAGTTTAAAGACTGATTTAA 981

QY 355 TyrGluArPgluAnThrArgTrIleCyvIleGlyProValaerPleuHisvMet 374
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Db 982 AAGAAATTGAATTAACGATTTCTTGATTAACACCTGTAAATCAAGCAATTTTGCGCC 1041

QY 375 LeuCyvSerTrpValGluArP---ProAnSerGluAlaPheYvLeuHisvLeuProArg 393
|||
Db 1042 CTGTGTAACCTTAATTAAGATGCTGTAGATTCAAAGCGCTTCAAAAGATTTCCAAATACGA 1101

QY 394 IleYvArPTrLeuTrpIleAlaGluArPgluMetYvMetGlnGlyTrpArPglYvSer 413
|||
Db 1102 TTCAAGATGCAATGTTTTCATAGGCCACAGGCGCATGACATTAAGGAAACCAAGGTGTG 1161

QY 414 GlnLeuTrpArPTrAlaPheAlaValGluAlaIleIleAlaSerAnPleuIleGly--- 432
|||
Db 1162 CAACCTGGAGCTGCTGCAATTTGCTCATTAATTTTCTGCTGCTGCTGCGCAAGAAAGA 1221

QY 433 ---GluPheGlyProThrIleArgYvAlaHisvThrYvIleYvArPArPTrValLeu 451
|||
Db 1222 CCGGAATTTTATTAACACATTTGCTCCGCTTAATAATTTCTGTGTCATGCTCAATTTGAC 1281

QY 452 GluArPcyv---ProGlyArPleuAnPleYvTrpYvArgHisvIleSerYvGlyAlaTrp 470
|||
Db 1282 ACTGAATGCGTTCTCTGTAGT-----TTTGAAGACAAAGAAAGGTGCTTGG 1329

QY 471 ProPheSerThrArgYvArPHisvGlyTrpProIleSerArPTrAlaGluGlyLeu 490
|||
Db 1330 GCTTTTCAAAAGAACTCAAGGTTATACGTTTCTGACTGATCGCAATTCATCAAG 1389

QY 491 AlaValLeuLeuLeu 495
|||
Db 1390 GCTATTAATCAATGTA 1404

RESULT 2

US-11-217-529-5565
; Sequence 5565, Application US/11217529
; Publication No. US2006099612A1
; GENERAL INFORMATION:
; APPLICANT: SUMTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OR INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5565
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5565

Alignment Scores:
Pred. No.: 5,15e-40 Length: 642
Score: 482.50 Matches: 91
Percent Similarity: 65.1% Conservative: 45
Best Local Similarity: 43.5% Mismatches: 68
Query Match: 11.6% Indels: 5
Gaps: 3

US-09-419-679-6 (1-757) x US-11-217-529-5565 (1-642)

QY 541 LeuGluIleLeuAnProAlaGluThrPheGlyArPrlleValIleArPTrProYvAl 560
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Db 1 ATGAGAACTTGAATCCAGCTGAAGTTTTCGTAACCTGCTAGCAATCCCATACCTG 60

QY 561 GluYvThrSerAlaAlaIleGlnAlaLeuAlaSerPheArgYvLeuYvTrpProGlyHis 580
|||

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Db      61 GAGTGCACAGATTTCTTCGTTCTTGACCTGACCTTACCTTCAATGTTTTTT---GACTAT 117
Qy      581 ArgatrglugluileglnhieCyelleaplysalathrthPheileglulyseilegin 600
Db      118 AAAAAAGGAAATCTCAACATGATTCAGAAATCGCTATTGAAATACATCAAGAAAGCTCA 177
Qy      601 AlaseapgysertrpyrglysertrpygllyvalCyephethrTYrglyalatrphPhe 620
Db      178 CTACACAGAGGAGGTGGATGAGAACTGGGGTATTGCTTCACCTATGACAGTATGTTT 237
Qy      631 GlyValIyvglyleuilealalealyargserPheSerPheSerlearglys 640
Db      238 GCGTGGAGACCTACACACTGTGGAGAAACATCGAAATTCCTCCAGCGGTGAGAAA 297
Qy      641 AlaCyglupheleuenseerlyseglneuproserglYglYtrpglygluserlyleu 660
Db      298 GGTGTGATTTCTCTGTGAGCAAGCAAGTGAAGACGCGTGGGTGAATCGATGAAG 357
Qy      661 SerCyglinaenlyvalYrseranleugluglyasnarSerHieValValanthr 680
Db      358 TCT-----AGTAGATTGATGATGATGATGATGATGATGATGATGATGATGATGAT 411
Qy      691 GlyTPAlameleuilealeupaleaplygllyalalealyargserleuproleu 700
Db      412 GCATGGGCACTGATTCGCTCTTTTGGCTGAATACCCGAAAGA-----AAGTCAAT 465
Qy      701 HieargAlaAlaAlaTytleuileanserglneugluapglYasPheProglnglu 720
Db      466 GACCAAGGATGACCTTTAAAGCATGACAGAAAGAAATCCGAGAAATGGAATTTGAG 525
Qy      721 GuilemerglYvalPheanlysaenCyemellethrTYrAlaAlaTYrarghanile 740
Db      526 ACCGTGAAGAGGTCTTTTAAATCATCTCTGTGCATGGAATCCAAAGTATATGATTTTG 585
Qy      741 PheproleletrpAlaLeuglyglutYr 749
Db      586 TTTCCTAATAAGCATTAAGTATGAT 612

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RESULT 3

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US-11-217-529-173919
; Sequence 173919, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 173919
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-173919

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Alignment Scores:

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Pred. No.: 9,53e-39 Length: 696
Score: 470.50 Matches: 94
Percent Similarity: 64.6% Conservative: 50
Beet Local Similarity: 42.2% Mismatches: 70
Query Match: 11.3% Indels: 9
DB: 7 Gaps: 4

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US-09-419-679-6 (1-757) x US-11-217-529-173919 (1-696)

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Qy      507 IleapVallysarlyleuTYrAspSerValasnValileuSerleuglnasn----- 524
Db      43 ATTAGCACTGACCGTTTATTTGAAGCATTAATGTTTATTTGAACCTACAAACCTCGGA 102
Qy      525 -----GluaperglyglYphealathrTYrgluueulyasrserTYrAsnTrpleuglu 542
Db      103 TCTTTGAATATNGTCTCTTTGCAACCTATGATAAATCAAGGCCCACTAGCAATGAA 162
Qy      543 IleileanProalagluThrPheglYasPleValileapTYrProTYrValGluCys 562
Db      163 ACCTGAATCTCGCTGGAAGTTTGTGTACATATGTGTAGATACCCATAGGTGAAGT 222
Qy      563 ThserAlaAlaileglAlaLeuAlasePhearharglyleuTYrProglYHieargYr 582
Db      223 ACTGATTAATCGTTCTGCGGTGACATATTTTACAAAG---TACTTGACATATGAAA 279
Qy      583 GlugluileglnhieCyelleaplysalathrthPheileglulyseileglnAlaser 602
Db      280 GAGGAATATCGTACACGATCAAGATCCCATCGCATTCATTAATAAATCTCAATTACA 339
Qy      603 AspglysertrpyrglysertrpygllyalCyephethrTYrglyalatrphPheglYal 622
Db      340 GATGGAAGTGTGATGAAAGCTGGGTATTGTTTACATATGCGGTATGTTTGCATVG 399
Qy      623 LyseglYleuilealalealyargserPheSeranCyserSerlearglyalCys 642
Db      400 GAGGATTAACACACCGTGGGAGACCTATGAAATTCCTCAACCGTAAAGAAAGCTTGC 459
Qy      643 GlupheleuenseerlyseglneuproserglYglYtrpglygluserlyleuSerCys 662
Db      460 GACTTCTGTCAGTAAACAGTGAAGATGCGGTTGGGGGAATCAATGAAGTCC--- 516
Qy      663 GlinaenlyvalYrseranleugluglyasnarSerHieValValanthrglYtrp 682
Db      517 ---AGTGAATTAATCATATGATGATGATGATGATGATGATGATGATGATGATGAT 573
Qy      683 Alameleuileuilealeaplygllyalalealyargserleuproleuhisarg 702
Db      574 GCGCTAATTTGCACTTTTCCCTGAATATCTTAATAA-----GAAGTCAATGACCGC 627
Qy      703 AlaAlaAlaTytleuileanserglneugluapglYasPheProglngluile 722
Db      628 GGTATTAACCTTTTAAATATGACAGAAATCCGGGGAATGGAATTTGAAGCTGA 687
Qy      723 MetglYval 725
Db      688 GAAAGTGT 696

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RESULT 4

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US-11-217-529-174234
; Sequence 174234, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174234
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-174234

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Alignment Scores:

Pred. No.:	8	78e-33	length:	1740
Score:	412.00		Matches:	750
Percent Similarity:	46.4%		Conservative:	25
Best Local Similarity:	37.4%		Mismatches:	89
Query Match:	9.9%		Indels:	10
DB:	7		Gaps:	60

US-09-419-679-6 (1-757) X US-11-217-529-174234 (1-750)

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Oy 1 metTPrLyLeuLeuPheAlaGluGluGlyAAsnProTPrLeuAlaGlnPheAAsnHis 20
    ::::::::::::::::::::
Db 52 CTTTGAGACCTAGGA-----ACTGATGAG 75

Oy 21 ValGlyArgGlnValTPrGluPhe-----AAsnProLyLeu 32
    ::::::::::::::::::::
Db 76 CTAGCCCGAGAAAGCTGGGAAATATTAAACCCCTCAGACAGCCGAAACAGCCACCATCC 135

Oy 33 GlySerProGlnAAsnLeuLeuGluTLeGluValAArgGlnAAsnPheHisAAsnAlaGly 52
    ::::::::::::::::::::
Db 136 ACTTCACGCAAGTGGCTTTCTTCAGATCCCAATTTCTCTCAACT--CATCCAGAAAG 192

Oy 53 PheThrHisLyHisSerAlaAAsnLeuLeuMetAArgMetGlnPheAlaArgGluAAsnPro 72
    ::::::::::::::::::::
Db 193 -----AAATACCATTCACCAAGATTT-----213

Oy 73 ThrArgGluValLeuProLyValGlyValLyAAsnTLeGluAAsnValThrGlnGluIle 92
    ::::::::::::::::::::
Db 214 -----TCA 216

Oy 93 ValThrLyLeuThrLeuAlaArgAlaValAAsnPheHisSerThrLeuGlnCyHisAAsnPro 111
    ::::::::::::::::::::
Db 217 GCCTTCGATGCGTGTCAATATGGTCGATCTTTTTCAACTGGTTCAGAGCCTGACTCA 276

Oy 112 GlnHisTPrProGlyAAsnTPrGlyGlyGlyProMetPheLeuMetProGlyLeuValHisThr 131
    ::::::::::::::::::::
Db 277 GGTATTTTTCCCGTCGCAATATAAAGACCCATGTCATAGACATGGTTATCGTAAGCCGTA 336

Oy 132 LeuSerTLeThrGlyAlaLeuAAsnThrValLeuThrGlnGluHisAArgLyGluIleCys 151
    ::::::::::::::::::::
Db 337 AACTATATCGCCGGT-----ATTGAATTCCTGACGATGAGAGAAATAGAAATTAAT 387

Oy 152 ArgTyrLeuTyrAAsnHisGlnAAsnLyS-----AAsnGlyTPrGlyLeuHisTLeGluGly 170
    ::::::::::::::::::::
Db 388 AGATACATCGTCAATATACAGCAGCATCCGGTTGATGGGGGCTGACATTTCTGTGAC 447

Oy 171 ProSerThrMetPheGlySerValLeuSerTyrTLeThrLeuAlaArgLeuGluGlyGlnGly 190
    ::::::::::::::::::::
Db 448 AAATCCACCGGTGTTGGTACAGATATGAACATAATGATCTTAATGGGTCTA---504

Oy 191 ProAAsnAAsnGlyGlnGlyGluMetGluValAArgAAsnTPrTLeuGluGlyHisGlyGly 210
    ::::::::::::::::::::
Db 505 CCCAAGGAC---CACCCGGTTGGCCGCAAGGACAGAGACATCTTTAAAGTTAGGCCGGT 561

Oy 211 AlaThrTyrTLeThrSerTPrGlyLyAsnMetTPrLeuSerValLeuGluValTyrGlnTPr 230
    ::::::::::::::::::::
Db 562 GCTATTGGATCCCTCAGCTGGGAGAAATTTGGCTTAAGTGCATTAACCTGATTAATAGG 621

Oy 231 SerGlyAAsnAAsnProLeuProGluTLeTPrLeuLeuProTyrMetLeuProPheHis 250
    ::::::::::::::::::::
Db 622 GAAGGTGTGAACCCGCGCCCTCGTAATCTGGTATCTTCATATTCAGTGGCCAGCAT 681

Oy 251 ProGlyAArgMetTPrCyHisAAsnAArgMetValTyrLeuProMetSerTyrTLeu 268
    ::::::::::::::::::::
Db 682 CCGGGAGAAATGGTGGTTCATCTAGAGAGTGTTAATCATCCGGTACGTAACCTGG 735

```

RESULT 5
US-11-217-529-166803
; Sequence 166803, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED

```

1  APPLICANT:  NAKAO, YOSHIHIRO
2  APPLICANT:  NAKAMURA, NORIHISA
3  APPLICANT:  KODAMA, YUKIKO
4  APPLICANT:  FUJIMURA, TOMOKO
5  APPLICANT:  ASHIKARI, TOSHIHIKO
6  TITLE OF INVENTION:  METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
7  FILE REFERENCE:  S-38-285
8  CURRENT APPLICATION NUMBER:  US/11/217,529
9  CURRENT FILING DATE:  2005-09-02
10 PRIOR APPLICATION NUMBER:  US 10/932,182
11 PRIOR FILING DATE:  2004-09-02
12 NUMBER OF SEQ ID NOS:  197023
13 SOFTWARE:  PatentIn version 3.3
14 SEQ ID NO 166803
15
16 LENGTH:  516
17
18 TYPE:  DNA
19
20 ORGANISM:  Saccharomyces pastorianus
21
22 US-11-217-529-166803

```

Alignment Scores:	
Pred. No.:	3 04e-11
Score:	195.50
Percent Similarity:	49.4%
Best Local Similarity:	35.5%
Query Match:	4.7%
DB:	7
length:	516
Matches:	61
Conservative:	24
Mismatches:	69
Indels:	18
Gaps:	5

US-09-419-679-6 (1-757) X US-11-217-529-166803 (1-516)

[illegible]

US-11-217-529-5615
RESULT 6
Sequence 5615, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NOBUHISA

```
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIRO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: S-38-285
/ CURRENT APPLICATION NUMBER: US/11/217,529
/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 5615
/ LENGTH: 5778
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-11-217-529-5615

Alignment Scores:
Pred. No. : 6.25 Length: 5778
Score: 100.50 Matches: 128
Percent Similarity: 34.8% Conservative: 92
Best Local Similarity: 20.2% Mismatches: 224
Query Match: 2.4% Indels: 190
DB: 7 Gaps: 30

US-09-419-679-6 (1-757) x US-11-217-529-5615 (1-5778)

QY 196 GYGLUMETGLUVALAARGAERTPLILEU----- 206
DB 3700 GGGGACCTTGAAMAAAATTGACGATATATCTAAAGACSTGTTGGATGCTTTAGCTACT 3759
QY 207 GYHIEGLYGLVALATHTYLIEHISERTTGPGLYUWERTTPEUSERVALLIUGLY 226
DB 3760 GGAATATATATATGCGAGTTACGCCAATAATTTGGTTAGGGCCTTGAGTATGCA 3819
QY 227 VALTYRGUUTPSEGLYASNAENPROLEUPROFGLUETLEUPEUPTGYMET 246
DB 3820 TTGGAATTTCCGTCCATGATGATTTCTTAATACGTCAGATTTTATTTTGGCTTCCAT 3879
QY 247 LEUPROPHENIAPROGLYARGMETTTPCYENIACYARGMETVALTYLEUPROMETSER 266
DB 3880 AGACACATAGATGCTAGTAATAATGTTGC-----AAA 3912
QY 267 TYLEUTYRGLYUYS-----ARGPHEVALGLYPROLIESERPROTHIVAL 281
DB 3913 ATACTATGGGAGCTAGGATTTAACTTTTGGAGAAATTTGGCTCTACAAACGCTTAA 3972
QY 282 LEUSERLEUARGLYUGLEUTYRTHIVAL-----PROTYRHIASERLLEAPR 297
DB 3973 AATGCATGCAATCCGAGGCTATTACAGTCATACCAATTTGGGAAACTTCATTTAAATGAT 4032
QY 298 TTPAERGLIALARGAENLEU-----CYEALILYSELIALSERLEUPTYRPROHISPROLEU 316
DB 4033 TAGCAATGGAGAGATTGCTCTTGTCTATTTTATATGATACATATTCAGAT----- 4086
QY 317 VALGLIAPRILEUTRPLASERLEUHIISYRHELEUGLUPROLILEU-----MET 334
DB 4087 -----TCAACACATTTTTCACGATGCAATGACSTTTTAAAGATTTGGCTTGGTTTAA 4143
QY 335 HIEETPRTGGLYUYSARGLEUARGLYULYENALILEIIESEERLALIEUGLUNHISILE-- 353
DB 4144 CAC-----ATTGTAATGAACTTTTCAAGATTTCCT 4173
QY 354 -----HIEYRGUUAERGLUADENH-----ARGTYRILECYSLIEGLYPROVALASN 369
DB 4174 AATCAAGAGAAATTGATGACGATGCAACGACGCTTATATA----- 4215
QY 370 LYEVALLIENWENMETLEUCYUETTPVALGLIUAERPROASERGLUALAPHELYS--- 388
DB 4216 -----GAAATGTTGAGATATCTGTTAGAGGCAACAGGCAAGATTTTCATATA 4266
QY 389 -----LEUHIISLEUPROARGILETYRERPTYLEUTRPLIENALIGLU 402
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DB 4267 ATGATTTACGATTTGTTGTCACATTTGTCAGAAAAGATTTGTTCAAGCCGCT--- 4323
QY 403 ASPGLYMETLYSMERGGLIYTYRASNLGYSEGLINLEUTTPAERTHIALAPHEALVAL 422
DB 4324 -----TTAAGCTCGAATCTTTTGGCAGGTACTATCGCATGGATGCTTATATGACACACTG 4377
QY 423 GINALIILEIIEALASERASNLEULEGLUGLUPHEGLYPROTHILARGYVALAHIS 442
DB 4378 GAAAGCATP-----CCATTT-----CCGCCCTGCCAGAACATATCT 4413
QY 443 THITYRILEYASNSERGLIVALIENGLUASPCYSPROGLYASPLEUASNLYSTPTPYR 462
DB 4414 TCGTTTGAAGAAAGAAATATTGCTTAAAGAACTGCA----- 4452
QY 463 ARGHISILIESERYGLYALATTPROPHESERTHIGLYASPHIAGLYTTPROLIESER 482
DB 4453 CGAAATTTTCCAGAGT----- 4470
QY 483 ASPCYSTHIALGLUGLYLEUYSALVALILEULEUUSERLYSILEALAPROGLUILE 502
DB 4471 -----CAAAACTAGAAAAGCTTTAGCTGTATACAG----- 4503
QY 503 VALGLYGLUPROIIASPVALLYSARGLEUTYRASPSEVALASNVALILEUSER--- 521
DB 4504 -----GACTTATTTAAGGCTTATGATGATGATCATCATATGACATTAAATGCT 4548
QY 522 -----LEUGLHASNGLUAPRGLY 527
DB 4549 TTGGCTTTTGTACACGACCAATAAGCTGATTTTACACGACGCTGAACTTTTGATATA 4608
QY 528 GLYPHEALITHITYRGUUEULYSARGSEPTYRANTTPLEUGLUILEIENPROLIA 547
DB 4609 CTGGTTCCAGCAT---TTCAAAATTTGTTATAGGATTTGGTCCCGAAATCTCA 4665
QY 548 GLUITHRPHIAGLYASRILEVALIILEAPRYRPTYRYVALIGLUCYTHISERILALALIE 567
DB 4666 AGAAATTAATCGTTATTTTTCGAAGCCCTTCATTTGAACACATTAACGTCATGACGAT 4725
QY 568 GINALIIEULASERPHIARGLYLEUTYRPROGLYHIARGARGGLUGLUILEGINHIS 587
DB 4726 AGGCTTTTAAAGAAATTATGACGATCTAATATATGATGACSTCTGCANAMAAATAGA-TAT 4784
QY 588 CYSLIAPRYALATHRPHIIEGLIULYSILEGIALASERASRGLYSERTPTRY 607
DB 4785 GCTATTTGATGAACCCCTCACT-----GGGGAATATCAT 4817
QY 608 GLYSERTTGPGLYVALCYSPHERHTYRGLYALATTPRPHIAGLYVALIYSELILEU-IIEAL 627
DB 4818 -----CATGTGCTCTCCGTAGAACCGGCTTTGAGCATATCCGATGACATACAAATAG 4868
QY 627 AALAGIARGSERPHESEYASNCSERSERIEARGLYVALIYSELILEU----- 643
DB 4869 TAGTGACAAAAGAAAGCTTATTAATAAACAAGTACCATGATGAAGAAACAGAACTT 4928
QY 644 -----PHIEULEUSERLYSGLINLEUPROSERGLYGLY-----TPRGL 656
DB 4929 GAGACACTTCAATTAATTTTCGAGCTTACCAAGAGCAAAAGGCTTACTGACCTGTGGGT 4988
QY 656 YGUISERTTYLEUSERCYEGLINLISYVALTYRSEYASNLIEUGLUGLYASNARGSERHI 676
DB 4989 AGAAGAGTATACCTATCATATCTAACAAACGTTCCCAACTTTATATG---AATIGATCAAG 5045
QY 676 SVALLIASENTHIGLYTPRALMETLEUVALIIEASRALIAGLYLIALYARGVAG 696
DB 5046 AGTTGTCAAAAGT-----ACTTAAACAA 5069
QY 696 PSEGLINPROLEUHIARGALIALALATYRLEUUILEASERGLIENGLUASRGLYAG 716
DB 5070 ACTTTCAACCGCTGAAATGCTATACGTTCCCTA-----GA 5105
QY 716 PRPHEPROGLINGLUILE-METGLYVALIYPHEASNLYSANCYSMETILETHR----- 733
DB 5106 AGTTAAGATGACGAATTAATAGGCTTG-----AAAACATGTGCATTAATACTTAA 5159
```

QY 734 -----TyrAlaAlaTyrArgSerIlePheProIleTyrA 745
DB 5160 AGATGACGAGATGTGACCAATTATTATAGGAGCTTTCGACAAATATTACCG----- 5212
QY 745 lAlaUgLYglUTyrGlnSerGlnValLeuGlnSer 756
DB 5213 -----GGACAATATCAGCCCGAGTTAATGAGGCA 5242
RESULT 7
US-11-217-529-5352
/ Sequence 5352, Application US/11217529
/ Publication No. US2006009612A1
/ GENERAL INFORMATION:
/ APPLICANT: SUNTORY LIMITED
/ APPLICANT: NAKAO, YOSHIHIRO
/ APPLICANT: NAKAMURA, NORIHISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIRO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: S-38-285
/ CURRENT APPLICATION NUMBER: US/11/217,529
/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO: 5352
/ LENGTH: 2466
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-11-217-529-5352
Alignment Scores:
Pred. No.: 2.7 Length: 2466
Score: 98.50 Matches: 160
Percent Similarity: 32.84 Conservative: 109
Best Local Similarity: 19.54 Mismatches: 291
Query Match: 2.44 Indels: 261
DB: 43 Gaps: 43
US-09-419-679-6 (1-757) x US-11-217-529-5352 (1-2466)
QY 17 LeuAaAmHleValIGLYArgGlnValTrrGlnPheAerProLYLeuGly----- 33
DB 1 ATGCACGAAATATGAAATGAGCAGAGAGACCTGTGAGCCAGCTGGAAATCTAACG 60
QY 34 -----SerProGlnAerLeuGlnIleGlnLYAlaArgGlnAer----- 47
DB 61 ATACACTGGCCCATGAAATTATCATGCAGCTCGMAAATGACAGTAAATAGGCAAAATG 120
QY 48 -----PheHisAerAaArgPheThiHisLeuHisSer 58
DB 121 TTCAAGGAATACGAGATGAAACGACCTTCCAGATTCAAGTTTCACTCGCAATTCGTA 180
QY 59 AlaAerLeuAerMetArgMetGlnPheAlaArgGlnAerProThiArgGlnValLeuPro 78
DB 181 GAGCTTACAAAT-----TCCGAGTCCCGTGAAGAAAGCTCCAAACATACATATTG--- 231
QY 79 LysValIGLYValLYAspRIleGlnAerValThrGlnGlnIleValThiLYeThrLeuArg 98
DB 232 -----AACAACTATAGCAGCGTCAATCATGAAAGTCCCTCAGATTCGCGGT 279
QY 99 ArgAlaValSerPheHisSerThiLeuGlnCysHisAerGlnHisTrrProGlnLYAspTyr 118
DB 280 ACCAACCGCTACATCGACCAAGAGGCTCAATGAAAGC-----TATTTCCTCGAATCGGT 336
QY 119 GLYGlyProMet-----PheLeuMetPro 126
DB 337 AGTGGCACTTACCAATGTTGGCGGCTACAGACAAAGTACTGAGTGGATCTGATAGTAAAC 396
QY 127 GLYLeuValIleThrLeuSerIleThrGlnLYAlaLeuAerThrValLeuThrGlnGlnHis 146

DB 397 GACCTGGTCAAGAGATTATCT-----GGTGTGCTAAAGAACCAACACCTTTAAAGGCAC 450
QY 147 -----ArgLYSerGlnIleCysArgTyrLeuTyrHisHisGlnAerLYAspGlyGlyTrr 164
DB 451 CTGAGATATGAAGAACAAATACTACCAACACGACGTGATGAAACAGAGAT----- 501
QY 165 GLYLeuHisIleGlnGlyProSerThiMetPhe-----GlySerValLeuSerTyrIleThr 183
DB 502 ACTATCAACATCTCAATTCGATAAAGATTCTTCAACCGCGGAAACGTCTCATATTGTTTCA 561
QY 184 LeuArgLeuLeuGlyGlyGlyProAaAerPheGlyGlnGlyGlnMetGlnLYValAerArgAer 203
DB 562 -----GATGACAGGATTCGGGCGCACAGCTGAAAGACATGACGTATTGAC 609
QY 204 TrpIleLeuGlnHisGlyGlyAlaThiTYrIle-----ThiSerTrrGlyLYs 219
DB 610 GGTATATTAAAAAACAATAATCGAACTATCTGATCGGGTCTCTTACAAACAGTAAACAG 669
QY 220 MetTrpLeuSerValLeuGlyValTyrGlnTrrPheGly-----AspAaerProLeuProPro- 238
DB 670 GCC-----AAGAAGAATGGTTTCGAACCGAGTCCGAT 705
QY 239 -----GlnIleTrrLeuLeuProLYrMetLeuProPheHisPrrGlyArgMetTrrCysHis 257
DB 706 TCGTTCAATTTTTCGCTTCGTCATCTA----- 733
QY 257 GCysArgMetValLYrLeuLeuProMetSerTyrLeuTyrGlyLYsAerPheValGlyProIle 277
DB 734 -TGTGTGCTGTCAAGCTC-----AATTCGGGT 759
QY 277 eSerProThrValLeuSerIleAerGlyGlyLeuTyrThiValProTrrHisAerIleAs 297
DB 760 GGAAGAACGA-----AATTATCGAAGAAACCCCACTAAACATATCCCGGGCCAA 813
QY 297 rTrrAerPrrAlaAerArgAerLeu----- 304
DB 814 TTGGGAATACAGATTCAACCATACGACGATGATGGACCCGCTTAAACCAAGGCTTAA 873
QY 305 -----CysAlaLYSerGlnAerLeuTrrTrrProHisPrrLeuValGlnAerIleLeuTrrAl 323
DB 874 GACGTGTCAAGTTCACACTCTCTG-----ACAAATCTTCTTCT 912
QY 323 aSerLeuHisIleAerPheLeuGlnPrrIleLeuMetHisTrrProGlyLYsAerGlyAerGly 343
DB 913 AATGATTCAACGTGATACGCTGCTGCTACCAAGATATCCAAAGACAGAAAGAACCG 972
QY 343 u-----LYsAlaIleIleSerAlaLeuGlnHisIleHisTrrGlyAerPrrI 358
DB 973 GCTTCGATTCTAAATATAAAGGCTTATGACTTCG----- 1006
QY 358 uAerThiArgTrrIleCysIleGlyProValAerLYsValLeu-----AspMetLeuCY 376
DB 1007 -----TCACCGAACAAGAGACCAACCAACCAAGAAAAAATG 1044
QY 376 GCysTrrValGlyAerProAerSerGlnAlaPheLYLeuHisIleLeuProArgIleTrrAs 396
DB 1045 CAA-GAAGAAATGAGAAACAAACAGATACCCCACTGGACACGCCAAATTCACACGA 1103
QY 396 rTrrLeuTrrIleAlaGlyAerGlyMetLYs-----MetGlnGly 409
DB 1104 TCTTTTAAAGAAATGAGCGGGAACAAAGGTTAAAGCAAGTGGCCAGCTTCGTTTC 1163
QY 409 YTrpAerGlySerGlnLeu-TrrAerPrrAlaPheAlaValGlnAlaIleIleAlaSerA 429
DB 1164 TATCTCAACTCAACCTGTGGAACAAC-----ATAAGAA 1199
QY 429 snLeuIleGlnGlyPheGlyProThiIleArgLYsAlaHisTrrTrrIleLYsAerSerG 449
DB 1200 ACTTA-----GAATTTCCCAACG-----AAAGGTCGA 1229
QY 449 InValLeuGlnAerCysPrrGlyAerPheAerLYsTrrTrrArgHisIleSerLYs----- 467

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Db 1230 AGATTACAGTCGATTTCG-----AAGTGACTCTTCATTCAAGAACTCGA 1277
Qy 468 -----GlyAlaTrpProPheSerThrGly-----AerHisG 478
Db 1278 AAGACAACTAGTATGATCTTAACAGTAAGCTG--TCCAGAACCCCGGCTCAGATTCCA 1336
Qy 478 1YTrp-----ProIleSerAspCysThrAlaGluGlyLeuVal 492
Db 1337 ACTGGGAAAAAATCCTGAAGTTTGACCTCTCCAACTGCMAA-----CTGAAAAACG 1387
Qy 482 aLLeuLeuLeuSerValIleAlaProGluIleVal----- 503
Db 1388 TTTTGGCTCGAAAGACTACTGCGCAACTTATGACGTTGAATTCGAATGCAAGAAC 1447
Qy 504 -----GlyGluProIleAspValIleAspValIleAspValIleAspValI 519
Db 1448 TGAGCAACCTTAGAGGGAATCCATCGCGTGTGAGCTGTTCGCTCAATTAACAGA 1507
Qy 519 IeLeuSerLeuGlnAsnGluAspGlyGlyPheAlaThrGlu--LeuValAspSer 538
Db 1508 TATCAAGCGCACACTGCTGCTTGTGGGTTGCGCGATCTGGAATGCTGATTTATCAT 1567
Qy 538 YAsnTrp-----LeuGluIleIleAsnProAlaGluThrPheGluAspIleVal 554
Db 1568 ACAACTACTTGAACACACAGCCTGAATTTCTGTGCGCTGCGCCACTTGCAAGATTA 1627
Qy 554 aLlLeAspTrpProTrpValGluCysThrSerAlaAlaIleGlnAlaLeuAlaSerPhe 574
Db 1628 ACCTCTCATATTAATCTATTACG-----TCCGTAGAGGGAATAGCACACTGCC 1675
Qy 574 rGlyLeuTrpProGlyHisArgArgGluGluIleGlnHisCysValIleAspValAlaThr 594
Db 1676 GCATCAAAAATGCAACTTTTCAGCAACGACATCCGCGCATCATCAT----- 1725
Qy 594 hrPheIleGluValIleGlnAlaSerAspGlySerTrpTrpGlySerTrpGlyValCysP 614
Db 1726 --TTGCGCGCACTGATCCAGACCAACACAGCGCGC----- 1758
Qy 614 heThrTrpGlyAlaTrpPheGlyValIleGlyLeuIleAlaAlaGlyArgSerPheSer 634
Db 1759 -----ATGGCGCGCTGTGACCGCTGCAAGTCTG-----GACTTAAGATTAACA 1804
Qy 634 snCysSerSerIleArgValaCysGluPheLeuLeuSerValGlnLeuProSerGlyG 654
Db 1805 ACATCAACGGGTGCAGAAC----- 1824
Qy 654 1YTrpGlyGluSerTrpLeuSerCys--GlnAsnValValTrpSerAsnLeuGluGly 673
Db 1825 -----ATCAACTGTCTGCCCATCTGAAGATTTTAACCTTGACCGCA 1867
Qy 673 sn-----ArgSerHisValValAsnThrGlyTrpAlaMet 685
Db 1868 ACCCGCTGTCTTCATCTGTCGAAAGCAACCAACCAACCGAATCTGACACTAGAGCTC 1927
Qy 685 euAlaLeuIleAspAlaGlyGlnAlaValAspArgAspSerGlnProLeuHisArgAlaAla 705
Db 1928 TTTCATCAAAAACACCGGAGGCGG-----CTGTCCAACTTACAA 1969
Qy 705 1aTrpLeuIleAsnSerGlnLeuGluAspGlyAspPheProGlnGlnGluIle 722
Db 1970 ACTACAGCTCAACACCAATACCTT-----TTCCCTTACCAAAACCTTA 2013

```

RESULT 8
US-11-217-529-80385
Sequence 80385, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:

APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHIISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO

```

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80385
; LENGTH: 2037
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80385

```

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:
Score:	2.27	2037	90	58	131
Percent Similarity:	98.00				178
Best Local Similarity:	32.4%				27
Query Match:	2.4%				
DB:	7				

US-09-419-679-6 (1-757) x US-11-217-529-80385 (1-2037)

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Qy 182 ILeThrLeuAspGlu-----LeuGlyGluGlyProAsnAspGlyGlnGlyGluMet 198
Db 925 TTGGTCTTAATTAATTAAGTCAACCTTTGGTGTAGTTTGTCTACTGATTAATTCGGTAAATTA 984
Qy 199 ---GluValAlaArgAspTrpIleLeuGlyHisGlyGly--AlaThrTrpIleThrSer 216
Db 985 CGGATTCATTTGAAGATTTCTGTGTAGTAATTTGGGAAATTCAGCAAAATTTCTGCGAG 1044
Qy 217 TrpGlyLysMetTrpLeuSerValLeuGlyValIlyGluTrpSerGlyAsnAsnProLeu 236
Db 1045 TATTCAGAGCCTGG-----TATGAG----- 1065
Qy 237 ProProGluIleTrpLeuLeuProTrpMetLeuProPheHisProGlyArgMetTrpCys 256
Db 1066 -----TCCTTTTGT 1074
Qy 257 HisCysArgMetValTrpLeuProMetSerTrpLeuTrpGlyLysArgPheValGlyPro 276
Db 1075 GGGTTTATTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1134
Qy 277 ILeSerProThrValLeuSerLeuArgGlyGluLeuTrpValProTrpHisAspIle 296
Db 1135 CTGGAAGCTAAGCTGCTAGACATTAACAAAT----- 1164
Qy 297 AspTrpAspGlnAlaArgAsnLeuGlyValGlyAspLeuTrpTrpHisProLeu 316
Db 1165 GATTTGGAAACA-----CCATGC 1182
Qy 317 ValGlnAspIleLeuThrAlaSerLeuHisLysPheLeuGluProIleLeuMetHisTrp 336
Db 1183 GTC--GACATCATTTAGTGTGAAGATCACTCAATTTA--CCGGTATAGGAATCTTTA 1236
Qy 337 ProGlyLysArgLeuArgGlyLysValIleIle-----SerAlaLeuGluHis 352
Db 1237 GATAGTTGACAGCAGCATTTACCGCTATGATTTGGAAGCAAAAGTTGATAGAGAAAT 1296
Qy 353 ILeHisTrpGluAspGluAsnThrArgTrpIleCysIleGlyProValAsnValLeu 372
Db 1297 ATTTTGAAGGTGCAAAAAAATAGC----- 1320
Qy 373 AsnMetLeuCysSerTrpValGluAspProAsnSerGluAlaPheLysLeuHisLeuPro 392
Db 1321 -----GATGATTATAGTAAGGAACAGCAAGAAATG--CTTGAA 1356
Qy 393 ArgIleTrpAspTrpLeuTrpIleAlaGluAspGlyMetLysMetGlnGlyTrpArgGly 412
Db 1357 GATCTATTCCTTAT-----AGGAATGATAGCATTCTATATGCTTAATTAGC 1404
Qy 413 -----SerGlnLeuTrpAspThrAlaPheAlaVal 422

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Db 1405 TTCGCTTTGAGTGTGTTCACTGGGTGATAGGAACATGCGCCGCTTGCCATTGGATTG 1464
Qy 423 GlnAlaIleIleAseRsnLeuIleGluIupheGlyProThrIleArgLysAlaHis 442
Db 1465 ATAGCTTATCTGCAACAGGG-----ACGAGAAAGTGA--- 1497
Qy 443 ThrTyrIleLysAseRsnGlnValLeuGluIupheCysProGlyAsePLeuAseLysTrpTyr 462
Db 1498 -----AGAAATGCTGATTCAGAAATTACTTCA----- 1527
Qy 463 ArgHisIleSerLysGlyAlaTrpProPheSerThrGlyAsePHis--GlyTrpProIle 481
Db 1528 -----CACTACCCATTGTTACGATGATGACATGATGATGATGCTA 1569
Qy 482 SerAsePThrAlaGluGlyLeuLysAlaValLeuLeuLeuSerLysIleAlaProGlu 501
Db 1570 AGTATATGTGTGAATGAGACTA-----CCAGAA 1599
Qy 502 IleValGlyGluProIleAsePValLysArgLeuTyrAsePVal----- 516
Db 1600 ATA-----GCCAAGGAATATATACACCGTGGTAAATCAATGTTA 1641
Qy 517 -----AenValIleLeuSerLeuGlnAseGluAsePglyGlyPheAlaThrTyrGlu 533
Db 1642 TCGGCACACAAATATGAAAGTATCGCAAAATTGTAAGGCG--GCCAAATATGAA 1698
Qy 534 LeuLysAseRsnTyrAsePTrpLeu----- 541
Db 1699 CTGTAAATGCTATCTGCTGCTATTTTGAAGCTTCGTCAGAGCGCCAGAAAGTTG 1758
Qy 542 -----GluIleIleAseP-----ProAlaGluThrPheGlyAseP 552
Db 1759 GACGACCCCTGTGTAATGCCATTGTGACAAAACTCCTCGCAGAG-----GATGAC 1812
Qy 553 IleValIleAsePTrpTyrValGluCys-----ThrSerAlaAlaIleGlnAlaLeu 570
Db 1813 GTTATTAATACCAACAAGACATTTAGATTGTAGTGAAGAAATTCATGCTCAAACTTTA 1872
Qy 571 AlaSerPheArgLysLeu-----TyrProGlyHisArgArgGluGlu 584
Db 1873 GCGGCATATGCTGTTCTGTCACAATTCTATGAGCTGAGGAGCAAGAGAT 1923

RESULT 9
US-11-145-307A-42
; Sequence 42, Application US/11145307A
; Publication No. US20060094035A1
; GENERAL INFORMATION:
; APPLICANT: Arcuturus Bioscience, Inc.
; APPLICANT: Erlander, Mark G.
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Identification of Tumors
; FILE REFERENCE: 022041-002020US
; CURRENT APPLICATION NUMBER: US/11/145,307A
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/577,084
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-145-307A-42

Alignment Scores:
Pred. No.: 2.25 Length: 1743
Score: 97.00 Matches: 42
Percent Similarity: 36.84 Conservative: 18
Best Local Similarity: 25.84 Mismatches: 59
Query Match: 2.34 Indels: 44
DB: 7 Gaps: 9
```

```
US-09-419-679-6 (1-757) x US-11-145-307A-42 (1-1743)
Qy 608 GlySerTrpGlyValCysPheThrTyrGlyAlaTrpPheGlyValLysGlyLeuIleAla 627
Db 34 GGGAAAGCGGGCGCCCTTTGGGCTCCAGGACGATTTGGAGCCCTCTGCTGTGGGA 93
Qy 628 AlaGlyAseRsnPheSerAsePValLeuGluIupheCysProGlyAsePLeuAseLys 647
Db 94 GAGAGCCGCGAGCGACGACCCCTGCTGCTCACTTGAGTGAAGACCGGCTTT----- 144
Qy 648 LysGlnLeuProSer-----GlyGlyTrpGlyGluSerTyr 659
Db 145 -----CCCGCAATCATGATCCTGATCTTTATTTGGGGGCTGGGAGAAAGATAT 195
Qy 660 LeuSerCysGlnAseLys-----ValTyrSerAseP-----LeuGluGly 672
Db 196 CTCAGCTGGGAAGAGACCGGGGCTCCGATTTGCTCTTCCAGCAGACCCGCTGAGTCT 255
Qy 673 AseArgSerHisValValAseP-----ThrGlyTrpAlaMetLeuAlaLeuIleAsePAlaGly 691
Db 256 GAACCATGACCTGACAGCAACCCCAAGAGTGAAGTGTGCTGCTACAGTGGCCGAGGT 315
Qy 692 GlnAlaLysArgAseRsnGlnProLeuHisArgAlaAlaAlaTyrLeuIleAseRsnGln 711
Db 316 CCC-----GATGCTTGATGATATCTCACCAGAGCCCG 348
Qy 712 LeuGluAsePglyAsePProGlnGlnGluIleMetGlyVal----- 725
Db 349 CTGGGCCAG--GATCCCGCGAGAGACAGTGTGAGGCTGCTACTGCAATGGGCGAG 405
Qy 726 PheAseLysAseP-----MetIleThrTyrAlaAlaTyrArgAseP 739
Db 406 TACAGAGAGACCTGTGCGCAGGGGATCACAAGAAATCAGGTATTTCTGATCAGAAAT 465
Qy 740 IlePhePro 742
Db 466 GCCCTTCCT 474

RESULT 10
US-11-217-529-75536
; Sequence 75536, Application US/11217529
; Publication No. US2006009612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75536
; LENGTH: 4179
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75536

Alignment Scores:
Pred. No.: 8.6 Length: 4179
Score: 97.00 Matches: 83
Percent Similarity: 32.7% Conservative: 42
Best Local Similarity: 21.7% Mismatches: 127
Query Match: 2.34 Indels: 130
DB: 7 Gaps: 20

US-09-419-679-6 (1-757) x US-11-217-529-75536 (1-4179)
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QY 219 LysMetTrpLeuSerValLeuGly-----ValTyrGluTrp----- 230
DB 2372 AAAAGATGGCTAGCTATGCTATGCTTCCCTTGAATGGATGATGATAAACAATTGA 2431
QY 231 -----SerGlyAenAsnProLeuProGlu---Ile 240
DB 2432 ATCCAAATGGTAAAGTTGATTAAGCCCTAACTTCATTCCTCCAACTCCCAAGCAATTAAAT 2491
QY 241 TTP-----LeuLeuProTyrMetLeuProPheHisProGly 252
DB 2492 TGGTAGCTGAAAAATACAGTTTCTGAAACAGCACTCAGATTACATGTTGAGCGCG 2551
QY 253 ArgMetTrpCysHisCysArgMetValTyrLeuProMetSerTyrLeuTyrGlyAsnG 272
DB 2552 AGGTTAGAGACTTATGATTAATATTAATCTTACCAAGCAGCATCTGTATACACAGATG 2611
QY 273 PheValGlyProIleSerProThrValLeuSerLeu----- 284
DB 2612 ATTCGTTTTCGATTTAAGGTGGTGCATCTTATCTTGGCTACCAAAATGATTTTACCTTAA 2671
QY 285 ArgGlyGluLeuTyrThrValProTyrHisAspIleAspTrpAspGlnIleArgAsnLeu 304
DB 2672 AGAAAAAGCTGCAAGTTGATTT--TACCAT-----TGGGCACAATTTTCAAGTATTC 2719
QY 305 CysAlaLeuGluAspLeuTyrTyrProHisProLeuValGln-----Asp 319
DB 2720 CAACGATTAAGGCCCTTTG-----CCGCGAAATTGACAGAAATTAATCATCGCGTGAT 2773
QY 320 IleLeuTrpAlaSerLeuHisCysPheLeuGluProIleLeuMetHisTrpProGlyLys 339
DB 2774 CATCTCAAGGTAGGTGCTCGAAATATGTCATCGCAAAATTAATGCGGAAGACCCCAAAAT 2833
QY 340 ArgLeuArgGluLysValAlaIleIleSerAlaLeuGlnHisIleHisTyrGlu----- 356
DB 2834 TGGTTAGACGCTACCAAGTCTGACCTCTCGAAGAAATTTTGTGAAACCTAATATAGTG 2893
QY 357 ---AspGluAsnThrArgTyrIleCysIleGlyProValAsnLysValLeuAsnMetLeu 375
DB 2894 CCGAGGAAAAAACAACATTAATGTGTTGTGTCAACCGGTGTCAACAGAGATTTTC----- 2944
QY 376 CysCysTrpValGluAspProAsnSerGluAlaPheLysLeuHisIleLeuProArgIleTyr 395
DB 2945 -----TGGGCT-----CCTACATCC----- 2959
QY 396 AspTyrLeuTrpIleAlaGluAspGlyMetLysMetGlnGlyTyrAsnGlySerGlnLeu 415
DB 2960 -----TTCAGATTTTGTAGAC----- 2977
QY 416 TrpAspThrAlaPheAlaValGlnAlaIleIleAlaSerAsnLeuIleGluIupheGly 435
DB 2978 -----GTTCTCCAAAGAACTACAGTTTCMAAGTGTGCCCCACGTCAGGG 3022
QY 436 ProThrIleArgGlyAlaHisIleThrTyrIleLysAsnSerGlnValLeuGluAspCys-Pr 455
DB 3023 CCAAGGATGAAGAAGCTGCAT-----TTGCAAGATTTGCAAA 3058
QY 455 OGlyAspLeuAsnLysTrpTyr----- 462
DB 3059 AGGCAAGTATCACTATGTAAGTTGGAACGAAAAATTTGCTCAAAATATTAAAGTTGAT 3118
QY 463 ---ArgHisIleSerLysGlyAlaTrpProPhe-----SerThrGlyAs 476
DB 3119 TAGGCGATTTATCTAAAGCCAAATTTGCTGCTTCAGATGAGAGTGATGATTTGGCAA 3178
QY 476 pHLeGly-----TrpProIleSerAsp-----CysThr 485
DB 3179 ACAAGTTGATATATATATTCATATATGATGATGCTGCTGCTTATTCATATGCA 3238
QY 485 rAlaGluGlyLeuLys-ALAValLeuLeuLeuSerLysIleAlaProGluIleValGlyG 505
DB 3239 AATTGAGGAGTCCAAATGTTATTTCAACTATCAATGTTATGAGCTTACCGCGCTCGGCA 3298
QY 505 IupProIleAspValLysArgLeuTyrAspSerValAsnValIleLeuSerLeuGlnAsn 525

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DB 3299 AGCCA-----AAAGTTCTTGACTTGTTCTCCACTTCTACTCTTGACACAG 3346
QY 525 lu 525
DB 3347 AA 3348

RESULT 11
US-11-217-529-551
; Sequence 551, Application US/11217529
; Publication No. US2006009612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 551
; LENGTH: 1692
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-551

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Alignment Scores:
Pred. No.: 2.72 Length: 1692
Score: 96.00 Matches: 82
Percent Similarity: 36.6% Conservative: 63
Best Local Similarity: 20.7% Mismatches: 129
Query Match: 2.3% Indels: 124
DB: Gaps: 20

US-09-419-679-6 (1-757) x US-11-217-529-551 (1-1692)

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```

QY 329 LeuGluProIleLeuMetHisTrpProGlyLysArgLeuArgGluLysAlaIleIleSer 348
DB 407 TTAGATTAACCTTATGGA-TATTGGGCGATGAAACAAACGCTGCCGAAACCTTAC--- 462
QY 349 AlaLeuGlnHisIleHisTyrGluAspGluAsnThrArgTyrIleCysIleGlyProVal 368
DB 463 ---GTTGATTAACATACTACCAAGATCCG-----TATTAAGTATGATGATTACAG 510
QY 369 AsnLysValLeuAsnMetLeuCysCysTrpValGluAspProAsnSerGluAlaPheLys 388
DB 511 CTCAAATATTAAATCAACCTCAGAGTGG-----GCACAAAAGTACGAG 555
QY 389 LeuHisLeuProArgIleTyrAspTyrLeuTrpIleAlaGluAspGlyMetLysMetGln 408
DB 556 CTAAAC-----GTTTGATTA-----GATTTACAT 579
QY 409 GlyTyrAsnGlySerGlnLeuTrpAspThrAlaPheAlaValGlnAlaIleIleAlaSer 428
DB 580 GGTGTTCCCGGATCCAAAAA-TGG-----GTTGCACACTCAGGCGAG 623
QY 429 AsnLeuIleGluIupheGlyProThrIleArgLysAlaHisIleThrTyrIleLys---Asn 447
DB 624 AATACTTTATGCGATTTGGG-----CTGGTTAAGATCAAAAGATATCGAAAACTAAC 677
QY 448 SerGlnValLeuGluAspCysProGlyAspLeuAsnLysTrpTyrArgHisIleSerLys 467
DB 678 TCTAGCAGTTTGGAGAAAAATGTTTGAACCTTCTTAATGATGATGAGCAAAAGCCCGCT 737
QY 468 GlyAlaTrpProPheSerThrGlyAspHisGlyTrpProIleSerAspCysThrAlaGlu 487
DB 738 GGTGGG----- 743

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QY 488 GlyLeuYsAlaValLeuLeuSer-LysrIleAlaProGluIleValGlyGluProI 507
DB 744 -----TCTGAAATCTCATGAGCCGCTCGGTGGTAAT 779
QY 507 eAspValYsArgLeu-----TyrAspSerValAsnValIleLeuSerLeuG 523
DB 780 TGAATATGCAATATAACAGACAGATGACTATGAAACATTGAC-----TATTCACAGA 833
QY 523 nAsnGluSerGlyGly---PheAlaThrTyrGluLeuYsArgSerTyr----- 538
DB 834 AAACCAAAATTCGGGTGACAAACAACTTTGTTATTCATGATGCTTTTCAAGCAGTCGG 893
QY 539 -AsnTrpLeuGluIleIleAsnPro----- 546
DB 884 CAATTGGAATTTAGACTGAAATCCGAATTTACCGCAATGTTTACAGCCATATTCAATT 953
QY 547 -----AlaGluThrPheGlyAspIleValIleAspTyrProTyrValGluCysTh 563
DB 954 GACTAAAGCGAATTATAGCTCTCAAGATATTCTAGTCGACCATCATTCATTACAGAGTCTT 1013
QY 563 rSerAlaAlaIleGlnAlaLeuAlaSerPheArgYsLeuTyrProGlyYHsArgArgG 583
DB 1014 TACACATTACAGCTGGCCGAAACTCAATTTTCAAGCT----- 1050
QY 583 uGluIleGlnHsCysIleAspYsAlaThrThrPheIleGluYsIle-----G 600
DB 1051 -----ATCGAAACAACTTATTAATTTATGGAATTTCCATACAAAGAGCTTCTTACCATCC 1106
QY 600 nAlaSerAspGlySerTyrGlySerTyrGlyValCysPheThrTyr----- 616
DB 1107 TGCAGTACTCGGGGAATGTTGGGTCATACCGATTGGCGCACCTGGTTGAATGGTGT 1166
QY 617 -----GlyAlaTrpPheGlyValYsGlyLeuIleAlaAlaG 629
DB 1167 GGGCGTGGGTGACAGCATATGATGGCTCTATATATATACGACACTGTTACACCCAGCAG 1226
QY 629 YArgSerPheSerAsnCysSerSerIleArgYsAlaCysGluPheLeuSerYsG 649
DB 1227 TAAACACAGCTGATCGTGTGCTCA-----CA 1253
QY 649 nLeuProSerGlyGlyTyrGlyGlySerTyrLeuSerCysGlnAsnYsValTyrSerAs 669
DB 1254 AAAACCTTAAAGCATTGACAGAGATTAC-----CGTATCGTGTACAGCATT 1304
QY 669 nLeuGluYsAsnArgSer-----HisValValAsnThrGlyTyr 682
DB 1305 CATCGAAGCACAAATTGGCCACCTATTCAACAAAGACGACTGGATGG 1350

RESULT 12
US-10-505-928-781
; Sequence 781, Application US/10505928
; Publication No. US20060088532a1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 781
; LENGTH: 6928
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-781

Alignment Scores:
Pred. No.: 23.5 Length: 6928
Score: 96.00 Matches: 113
Percent Similarity: 29.84 Conservative: 71

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Best Local Similarity: 18.3% Mismatches: 196
Query Match: 2.3% Indels: 238
DB: 6 Gaps: 35

US-09-419-679-6 (1-757) x US-10-505-928-781 (1-6928)
QY 103 PheHisSerThrLeuGlnCysHsAspGlyYHsTrpProGlyAspTyrGlyYsProMet 122
DB 513 TATCATGAG---ATCTATACAGAGATGGGAGAC-----TCTATGGAGACCTTGT 560
QY 123 -----PheLeuMetProGlyLeuValIleThrLeuSerIleThrGlyAlaLeuAsn 139
DB 561 GAATTCATCTTAAATGATGAG---ACCTGCATCATGAT 599
QY 140 ThrValLeuThrGluGluHsArgYsGluIleCysAspArgTyrLeuTyrAsnHsGlnAsn 159
DB 600 TGCATTTCTGATGAAAGATACATAGTGGCCATGGTGCCACCACTTAATATGAA--- 656
QY 160 LysAspGlyGlyTyrGlyLeuHsIleGlu-----Gly 170
DB 657 TATGACCGAAAGTGGGCATCTGCTTAAAGCCTGAAAACGTTGTGAAGATATTGGGAA 716
QY 171 ProSerThrMetPheGlySerValLeuSerTyrIleThrLeuArgLeuGlyGlyGly 190
DB 717 AAGAAGCAGCAGTTTGGAAAGTTGCTACCAATTTAATCT----- 755
QY 191 ProAsnAspGlyGlnGluMetGluYsAlaArgAspTyr----- 204
DB 756 -----CAGACGGCTCTTTCTTGAAAGAAAGCTTATGTTTCA 791
QY 205 -----IleLeuGlyHsGlyGlyAlaThrTyrIleThrSerTyr 217
DB 792 TGTGCAATCAAGAGCTGATTTACTGACATCAACAGCTGCTGTAATTAATCTTACTT 851
QY 218 GlyYs-----MetTrpLeuSerValLeuGlyValTyr----- 228
DB 852 AAAGAAAGAAAGCATTGCTAAGATTCTTGGATGGTTTAAATCAGATATCTTACTT 911
QY 229 -----GluTrpSerGlyAsnAsnProLeuProProGluIleThrLeuLeuProTyr 245
DB 912 AGAGCTGGGAATGTGACAGCAACAAACATTA-----AAC 947
QY 246 MetLeuProPheHisProGlyArg----- 253
DB 948 TTTTCACTGGGATCCAGACAGGCCAGTGCACCTATAGTGCTCCAGCTGCA 1007
QY 254 -----MetTrp-----CysHsCysArgMetValTyr 262
DB 1008 AGATGATGCTGAGTCTGGTCTGTGGCAGAGCTTTTCTGTGAAGCTCAACCTCCAT 1067
QY 263 LeuProMetSerTyrLeuTyrGlyYsArgPheValGlyProIleSerProThrValLeu 282
DB 1068 GTTCGACAGAAA-----CCATTAAATATACAGTG--- 1097
QY 283 SerLeuArgYsGluLeuTyrThrVal---ProTyrHisAspIle----- 296
DB 1098 -----GAGTTAAACAGATGTGACATCTCAAGATACCCGCTGTATGCAGGC 1145
QY 297 -----AspTrpAspGln 300
DB 1146 TGGCTGCCAAATAATGATTTTGTCTATCTGCTGTAATAGAAATATCTCGGAGATAG 1205
QY 301 AlaArgAsnLeuCysAla-----LysGluAspLeuTyrTyrProHisProLeu----- 316
DB 1206 GCACATCGAAATGCAAGAGCTTTCAGTAGTACCTTAATCAGCAATTCATCTCTGACAGAT 1265
QY 317 -----ValGlnAspIleLeuThrAlaSer 324
DB 1266 GTGAGGTGGTTGTCAAAAATCCCATATAGAGATATCAAAAGAAAGATGTGAGTGGC 1325
QY 325 LeuHisYsPheLeuGluProIleLeuMetHisTrp---ProGlyYsArgLeuArgGlu 343
DB 1326 CTTAAGAACATTAACATCACTTATTTTCAGTGTGCAAGATGTTACTGAAGTTACT--- 1382

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Qy 344 LyvalalleleseralaleuGluhiwlehiwtyrgluabpGluabn----- 359
Db 1363 -----CTAACATATTGGAGATGAGAAATGACCAATGTT 1415
Qy 359 ----- 359
Db 1416 CCTTACATAGACGCCCACTGTGTTCTTACTTACAGAGCTAGCTAGTGGAAAGTC 1475
Qy 360 -----ThragtyrileGysileGlyProvalabnyval----- 371
Db 1476 CAATCATGTGAGAGAACTAAATATGTATGCAAGAAAGAGAAATCTGAAATGAC 1535
Qy 372 -----LeuabmetleuGysytrValGluabpProabnserGluabPheyluleu 389
Db 1536 GCAAGTTCGATAGATGTGT-----CTCCAGATGAGGCTGGAAAGAGA 1580
Qy 390 HleuProatrglletyrbpTyrlleuTrpillealGluabpGluabPheyluleu 409
Db 1581 CATGAGAAACCTGTACAAAG-----ATTATGAGAGATGAGGTCCCTTTT---GGA 1628
Qy 410 tyrbpGlyserGluabPheyluleuTrpabPheyluleuValGluabPheyluleu 429
Db 1629 ACAAACTGCAATCTGATCTACTAGCAAGATTTGACCAAGAAATGCTA-----AATGAT 1682
Qy 430 LeuileGluabPheyluleuProthyleatrglyvalahlethtyrileGluabnserGlu 449
Db 1683 TTGATGAAAAAGATGATTAATCTGAAAGAAA-----TACTTTCGAACTGGCCTG 1733
Qy 450 valleuGluabPheyluleuProthyleatrglyvalahlethtyrileGluabnserGlu 463
Db 1734 AGAGATGATGATCTGTGGAGAGATTAAC---TGGGCAACTGTGTGGAGAAAGCCG 1790
Qy 464 HleileserlyleGlylatrProPhe----- 472
Db 1791 GCTGATCACTTCCAACTGGAAATTTCTTGGACCCAGCTTCCCGGAGCCTCGTGCT 1850
Qy 473 ---SerthrglyabPheyluleu-----GlyTrpProileserabPheyluleuGluab 489
Db 1851 ATGTCATGGAAGTCTGTGGAAAGTGGAGAGTGAAGACGCTG-----AGAGCTTC 1904
Qy 490 LyvalValleuLeuLeuSerlylealProGluileValGluabPheyluleu 509
Db 1905 AAAGCACTTCATTTGCAAGAAATGAGTGAACCCCTGGCCTGGAAGAAAGTCCCT 1964
Qy 510 lye-----ArgleutyrbpserValabnyValleuLeuLeu 523
Db 1965 AAGCTGATGACCCCTGCTCTGAAGGCTGGCAAGTTTCCCGCAAGCTTTCTGTTAT 2024
Qy 524 AbnGluabpGlylePhealserThrglyleuLeuLeuLeuLeuLeuLeuLeu 543
Db 2025 AAGGTA-----TTCCATGCAAGAAAGATTTGAAGAAAGAACTGGAAAGCT 2075
Qy 544 lleaabProalagluThrPheGlyabPheyluleuValleuLeuLeuLeuLeu 561
Db 2076 GAAGCATTCGCCAAGCCCTTGGAGCAACCTTCTGATTCAGCCATGTGAT 2129

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RESULT 13
US-11-217-529-3854
; Sequence 3854, Application US/11217529
; Publication No. US2006009612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182

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; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3854
; LENGTH: 2586
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3854

Alignment Scores:
Pred. No.: 7.38 Length: 2586
Score: 94.50 Matches: 120
Percent Similarity: 32.2% Conservative: 52
Best Local Similarity: 22.5% Mismatches: 156
Query Match: 2.3% Indels: 207
Gaps: 27

US-09-419-679-6 (1-757) x US-11-217-529-3854 (1-2586)
Qy 120 GlyPrometPheleuMetProGlyleuVallethryleSerilethrglyAlaleuabn 139
Db 911 GGGTCTTTTGAACCTTTGGCCCTTGGCAAGATTAACATTCCTGCTGAGCTTGAACCAT 970
Qy 140 ThrValleuThrgluGluhiabrglyleuGlyCysatrglyLeuTyrbpAbn 159
Db 971 GTC-----AAGATTGCTGCAAAAAAGTTTACAGAAACATG- 1008
Qy 160 lyaabpGlyGlyTrpGlyleuhiwleGluGlyProserThmetPheGlyserValleu 179
Db 1009 AAG-----TATAGACTGTGATGCTGTTTAC 1035
Qy 180 SerTyrlleThleu-----ArgleuLeuGlyGluGlyProabn 193
Db 1036 ACTTTCTACTCTCTTTTGGAGCAAGATCTCTCAATATTTTGAAGAGTTAAAGAC 1095
Qy 194 GLyngluGluMetGluValabrgabPhePhe-----leuGlyhiwleGlyAla 211
Db 1096 AATAGCCCAAGCTCTTAATGAGAAAGATGGTTGCCAAATTTACAGCCACATGCGG 1155
Qy 212 ThrTyrbp-----lethserTrpGlyleuSerValleuGlyValGlyGlu 229
Db 1156 ACATTTGAATCTTTAGTAATTCACATGATATATCTTAATGATCTACATTAAGGCAA 1215
Qy 230 TrpSerGlyabnabnProleuProGluileThrPheleuProTyrbpMetleuProPhe 249
Db 1216 -----GACCTCATGTGTGTGAGATGATGATAAGATGAGTGGCTTTTACAAGA 1263
Qy 250 HlePro-GlyabrgmetTrpGlyhiwleCysatrgMetValTyrlleuProMetSerTyrlleu 269
Db 1264 AACCTGCGCGCAAAATGATGATATATGCAAG----- 1295
Qy 269 yrcGlylyab-ArgPheValGlyProileserProthValleuSerleuabrglyleu 288
Db 1296 ---GGCCGTATGAAAGTTGATCTCTCAAGTAAAGAACCCCGGTTCTTTGGTAAAGTA 1353
Qy 289 TyrbpValProTyrbpPheyluleuPheyluleuPheyluleuPheyluleu 303
Db 1354 TGGCGCTA---TATGAGATCTGTATGGATTAAGAAAGCCACTAGTACAGCAAGGAG 1410
Qy 304 LeuCyAlaValabPheyluleuTyrbpProhiwleProleuValGluabPheyluleu 323
Db 1411 TTATGGCA---CAGGCTGAAAGTACATTTCTTGTTCATGAT----- 1455
Qy 324 SerleuhiwleabPheleuGluProileleuMetThrProGlylyabrgleuabrglu 343
Db 1456 -----CTGGAAGAAATTTATTAACCTGGCGTGAAGAAAGATTAAGCAAC 1500
Qy 344 LyvalalleleseralaleuGluhiwlehiwtyrgluabpGluabPheyluleu 363
Db 1501 GAAGCAAT-----GAGGAAAGCAAT 1521
Qy 364 CysilleglyProvalabnyValleuabmetleuGysytrValGluabPheyluleu 383

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Db      1233  ----TGGGTGCCCCCTTTGATGATGGGAAAGTCTTATCATACCAAGGAGCAAGCTTG 1288
Qy      217  |||||-----LysMetTyrPheLeuSer----- 223
Db      1289  GGGGGTTTGGCCAAACCTTCACAGAGTGTGAGGGGAGAGGCTGTGGGATCAAGAAGCTTC 1348
Qy      224  -----ValLeuGlyValTyrGluTyrSerGlyAsnAsnProLeuProProGluIuI 240
Db      1349  GGCTACCTCCCTGTACAGGACGCTTGATGATGAGGAAACCAATACCTTG-----ACCTG 1402
Qy      240  eTTPLeuLeuProTyrMetLeuPro----- 248
Db      1403  CTGGTGGGCTCCCTGTGACACCGCATGCTTTCAGGGCCAGACCCATCTCCATGTC 1462
Qy      249  -----PheHisProGlyArgMetTyrCysHisCysArgMetValTyr 262
Db      1463  TCCCATGAGGTCTCTATTGCTCCACAGACATCGACCTGAGC----- 1505
Qy      262  rLeuProMetSerTyrLeuTyrGlyLysArgPheValGlyProIleSerProThrValIle 282
Db      1506  -----AGCCCAACTGTGCT 1519
Qy      282  uSerLeuArgLysGluLeuTyrThr 290
Db      1520  GGGCGGCACTCGGTCTGTGTGAGCC 1544

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RESULT 15

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US-10-505-928-151
/ Sequence 151, Application US/10505928
/ Publication No. US20060088532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ludwig Institute for Cancer Research et al.
/ TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
/ FILE REFERENCE: 28967/39178
/ CURRENT APPLICATION NUMBER: US/10/505,928
/ PRIOR FILING DATE: 2004-08-27
/ PRIOR FILING DATE: 2002-03-07
/ NUMBER OF SEQ ID NOS: 866
/ SOFTWARE: PatentIn 3.2
/ SEQ ID NO 151
/ LENGTH: 128361
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-505-928-151

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Alignment Scores:

```

Pred. No.: 3.28e+03 Length: 128361
Score: 94.00 Matches: 78
Percent Similarity: 30.7% Conservative: 28
Best Local Similarity: 22.6% Mismatches: 118
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US-09-419-679-6 (1-757) x US-10-505-928-151 (1-128361)

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Db      83836  AAAACAAACAAACAAACATACAAACAAACAAACAAACAAACAAATATGCAAGTTGG 83895
Qy      115  ProGlyAspTyrGlyGlyProMetPheLeuMetProGlyLeuVal----- 129
Db      83896  GAGAGACCAAGAGAGAGCTCCCTCTACTCTCCCAAGCCTGATCTGAATGGAGAGAGC 83955
Qy      130  -----LThrLeuSerLLeThrGlyAlaLeuAsnThrValLeuThrGluGluHis 146
Db      83956  CTGTGAGAGCTGCTGCTGCTCA-GTGGAGAGCTGTGCTGCAACCCAGCACTGCTCCCA 84014
Qy      147  ArgLysGluLeuLeuCysArgTyrLeuTyrAsnHisGlnAsnLysAspGlyLysTyrGlyLeu 166
Db      84015  ---TCACCTGTGCTCAGGTACGGCTTG---CATCCCTGTACTCTCTCCGGGGGTGGTCCC 84068

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Qy      167  HisIleGluGly-----ProSerThrMetPheGlySerValLeuSer 180
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Qy      181  TyrIleThrLeuArgLeu----- 186
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Qy      187  -----LeuGlyGluGlyProAsnAspArgLysGluGlyMetGlu 199
Db      84188  GCTCCAGGTGTACAGACACCTTGGAGCTCTCTCTGTGACGGCGAGAGATGTGCT 84247
Qy      200  LysAlaArgAspTyr-----IleLeuGlyHisGlyAlaThrTyrIleThrSerTyr 217
Db      84248  GAGCCAGAGAGAGCTGCTGCTCTCTTGGCCGAGAGAGCTCCGGGTATGAGAGGAACCTG 84307
Qy      218  GlyLysMetTyrPheSerValLeuGlyValTyrGluTyrSer-GlyAsnAsnProLeuPr 237
Db      84308  GGTGCAATTGTGG-----GGTGCCTCTCCCTGTGATGACCTCTCTCCCTGCC 84355
Qy      237  oProGluIleTyrPheLeu-----ProTyrMet 246
Db      84356  ACCCCACACCTGGCTTTGACGCTTGAGCTGCTGACCTCCAGCCCAAGCCACCAT 84415
Qy      246  r-----LeuProPheHis-----ProGlyArgMetTyrCysHis 257
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Qy      270  yLysArgPheValGlyProIleSerProThrValLeuSer----- 283
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Qy      290  rValProTyrHisAspTyrAspTyrAspTyrAspTyrAspTyrAspTyrAspTyrAspTyr 310
Db      84710  TGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 84749
Qy      310  uTyrTyrProHisProLeuValGlnAspTyrLeuTyrPheLeuHisLysPheLeuGlu 330
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Qy      330  uProIleLeuMet 334
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Search completed: May 22, 2006, 22:49:07
Job time : 144 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: May 22, 2006, 22:10:00 ; Search time 1956 Seconds
(without alignments)
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Searched: 18892170 seqs, 6143817638 residues
Total number of hits satisfying chosen parameters: 37784340

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	4148	100.0	2560	8	US-10-607-726-5

2	3480	83.9	2280	3	US-09-938-842A-833	Sequence 833, App
3	3480	83.9	2280	3 <th>US-09-938-842A-833</th> <th>Sequence 833, App</th>	US-09-938-842A-833	Sequence 833, App
4	3248	78.3	2776	3 <th>US-10-425-115-91064</th> <th>Sequence 91064, A</th>	US-10-425-115-91064	Sequence 91064, A
5	3240.5	78.1	4120	8 <th>US-10-437-963-71137</th> <th>Sequence 71137, A</th>	US-10-437-963-71137	Sequence 71137, A
6	3237	78.0	2638	9 <th>US-10-425-114-25096</th> <th>Sequence 25096, A</th>	US-10-425-114-25096	Sequence 25096, A
7	3237	78.0	2786	9 <th>US-10-425-115-90182</th> <th>Sequence 90182, A</th>	US-10-425-115-90182	Sequence 90182, A
8	3234	78.0	2355	8 <th>US-10-437-963-71159</th> <th>Sequence 71159, A</th>	US-10-437-963-71159	Sequence 71159, A
9	3181.5	76.7	2653	8 <th>US-10-425-114-24593</th> <th>Sequence 24593, A</th>	US-10-425-114-24593	Sequence 24593, A
10	3125	75.3	2558	8 <th>US-10-607-726-1</th> <th>Sequence 1, Appl1</th>	US-10-607-726-1	Sequence 1, Appl1
11	2756	66.4	2271	16 <th>US-11-096-568A-30648</th> <th>Sequence 30648, A</th>	US-11-096-568A-30648	Sequence 30648, A
12	2551	61.5	2538	7 <th>US-10-221-074-7</th> <th>Sequence 7, Appl1</th>	US-10-221-074-7	Sequence 7, Appl1
13	2543.5	61.3	2593	9 <th>US-10-425-114-24645</th> <th>Sequence 24645, A</th>	US-10-425-114-24645	Sequence 24645, A
14	2543.5	61.3	2627	9 <th>US-10-425-115-65768</th> <th>Sequence 65768, A</th>	US-10-425-115-65768	Sequence 65768, A
15	2541	61.3	2669	8 <th>US-10-424-599-35539</th> <th>Sequence 35539, A</th>	US-10-424-599-35539	Sequence 35539, A
16	2538	61.2	2478	7 <th>US-10-221-074-3</th> <th>Sequence 3, Appl1</th>	US-10-221-074-3	Sequence 3, Appl1
17	2538	61.2	2478	7 <th>US-10-427-570A-4</th> <th>Sequence 4, Appl1</th>	US-10-427-570A-4	Sequence 4, Appl1
18	2538	61.2	2478	16 <th>US-11-076-733-18</th> <th>Sequence 18, Appl</th>	US-11-076-733-18	Sequence 18, Appl
19	2538	61.2	2567	8 <th>US-10-425-114-7892</th> <th>Sequence 7892, Ap</th>	US-10-425-114-7892	Sequence 7892, Ap
20	2522.5	60.8	2545	16 <th>US-11-096-568A-24178</th> <th>Sequence 24178, A</th>	US-11-096-568A-24178	Sequence 24178, A
21	2522.5	60.8	2574	9 <th>US-10-739-930-2894</th> <th>Sequence 2894, A</th>	US-10-739-930-2894	Sequence 2894, A
22	2516.5	60.7	2093	7 <th>US-10-259-194A-115</th> <th>Sequence 115, App</th>	US-10-259-194A-115	Sequence 115, App
23	2454.5	59.2	2731	7 <th>US-10-221-074-1</th> <th>Sequence 1, Appl1</th>	US-10-221-074-1	Sequence 1, Appl1
24	2436	58.7	2746	8 <th>US-10-424-599-31007</th> <th>Sequence 31007, A</th>	US-10-424-599-31007	Sequence 31007, A
25	2436	58.7	2766	7 <th>US-10-221-074-5</th> <th>Sequence 5, Appl1</th>	US-10-221-074-5	Sequence 5, Appl1
26	2436	58.7	2766	7 <th>US-10-427-570A-1</th> <th>Sequence 1, Appl1</th>	US-10-427-570A-1	Sequence 1, Appl1
27	2436	58.7	2766	16 <th>US-11-076-733-19</th> <th>Sequence 19, Appl</th>	US-11-076-733-19	Sequence 19, Appl
28	2433	57.0	1882	8 <th>US-10-607-726-3</th> <th>Sequence 3, Appl1</th>	US-10-607-726-3	Sequence 3, Appl1
29	2363.5	56.8	2416	8 <th>US-10-424-599-35538</th> <th>Sequence 35538, A</th>	US-10-424-599-35538	Sequence 35538, A
30	2354.5	56.4	2457	7 <th>US-10-168-445-14</th> <th>Sequence 14, Appl</th>	US-10-168-445-14	Sequence 14, Appl
31	2339.5	56.4	2319	8 <th>US-10-425-114-1854</th> <th>Sequence 1854, Ap</th>	US-10-425-114-1854	Sequence 1854, Ap
32	2339.5	56.4	2379	9 <th>US-10-425-115-90180</th> <th>Sequence 90180, A</th>	US-10-425-115-90180	Sequence 90180, A
33	2336	56.3	2484	8 <th>US-10-425-114-10317</th> <th>Sequence 10317, A</th>	US-10-425-114-10317	Sequence 10317, A
34	2336	56.3	2500	8 <th>US-10-424-599-4661</th> <th>Sequence 4661, Ap</th>	US-10-424-599-4661	Sequence 4661, Ap
35	2311.5	55.7	2067	7 <th>US-10-429-949-6</th> <th>Sequence 6, Appl1</th>	US-10-429-949-6	Sequence 6, Appl1
36	2264	54.6	2510	8 <th>US-10-425-114-24639</th> <th>Sequence 24639, A</th>	US-10-425-114-24639	Sequence 24639, A
37	2256.5	54.4	2415	9 <th>US-10-739-930-740</th> <th>Sequence 740, App</th>	US-10-739-930-740	Sequence 740, App
38	2226.5	54.1	2526	9 <th>US-10-425-115-44214</th> <th>Sequence 44214, A</th>	US-10-425-115-44214	Sequence 44214, A
39	2226.5	54.1	2526	8 <th>US-10-425-114-9157</th> <th>Sequence 9157, Ap</th>	US-10-425-114-9157	Sequence 9157, Ap
40	2097.5	50.6	2432	8 <th>US-10-437-963-100852</th> <th>Sequence 100852, A</th>	US-10-437-963-100852	Sequence 100852, A
41	2083	50.2	2639	8 <th>US-10-389-566-248</th> <th>Sequence 248, App</th>	US-10-389-566-248	Sequence 248, App
42	2070.5	49.9	1939	8 <th>US-10-425-114-10363</th> <th>Sequence 10363, A</th>	US-10-425-114-10363	Sequence 10363, A
43	2060.5	49.7	2182	8 <th>US-10-424-599-139406</th> <th>Sequence 139406, A</th>	US-10-424-599-139406	Sequence 139406, A
44	1959	47.2	2414	9 <th>US-10-425-115-171124</th> <th>Sequence 171124, A</th>	US-10-425-115-171124	Sequence 171124, A
45	1882	45.4	1546	7 <th>US-10-259-194A-548</th> <th>Sequence 548, App</th>	US-10-259-194A-548	Sequence 548, App

ALIGNMENTS

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; Publication No. US20040121439A1
; GENERAL INFORMATION:
; APPLICANT: Falco, S. Carl
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Rafalski, Antoni
; APPLICANT: McGonigle, Brian
; APPLICANT: Lohman, Karin
; TITLE OF INVENTION: Enzymes Involved In Squalene Metabolism
; FILE REFERENCE: BB1113 US NA
; CURRENT APPLICATION NUMBER: US/10/607,726
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/419,679
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/105,405
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 2560
; TYPE: DNA

ORGANISM: Glycine max
US-10-607-726-5

Alignment Scores:

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Best Local Similarity:	100.0%	Mismatches:	0
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US-09-419-679-6 (1-757) x US-10-607-726-5 (1-2560)

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QY 61 LeuLeuMetArgMetGlnPheAlaArgGluAsnProThrArgGluValLeuProLyVal 80

DB 205 CTACTTAATGCCGATGCAAGTTCGACAGAGAGAACCCACACGTAAGTCTTCGCCAAATC 264

QY 81 GlyValLyAspPLeGluAspValThrGlnGluLeuValThrLyThrLeuArgArgAla 100

DB 265 GGAAGTTAAGATATATGAGGATGTGACCAAGAGATTGTGACAAACATTAAAGAGGCGC 324

QY 101 ValSerPheHisSerThrLeuGlnGlyHisAspGlyHisSTPrProGlyAspTPrGly 120

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QY 121 PrometPheLeuMetProGlyLeuValIleThrLeuSerIleThrGlyAlaLeuAsnThr 140

DB 385 CCCATGTTTCTGATGCTCGCTGGCTGGTGAATTAATCTCTGTCTATCACTGGGGCGTTGAAATCA 444

QY 141 ValLeuThrGlnGluHisArgGlySerGlyIleCyAspArgTyrLeuTyrAsnHisGlnAsnLy 160

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Db      2065  GGGTGGGCTATTTGGCTCTCTATTGCTGACAGGCTTAAAGATTCGCAACACAG 2124
Qy      701  HIsArGAlaAlaAlaTyrlLeuIleAerSerGlnLeuGluAerGlyAerPheProGlnGln 720
Db      2125  CACGGGGAGCTGCACTATTGATTAATCCCAATTGAGAGCGGTGACTTTCGCGACAG 2184
Qy      721  GIuIleMeGlyValPheAerAerAerSerGlnIleThyTyrlAlaAlaTyrlAerGlnIle 740
Db      2185  GAAATTAATGGAGTCTTCAACAAGATTCATGATCACTACCGCATACAGAAACATA 2244
Qy      741  PheProIleTPAlaLeuGlyGluTyrlGlnSerGlnValIleGlnIleSerArg 757
Db      2245  TTCCCATTTGGGCGTTGGGAAGATTCCAATCCCAAGTATTGCAATCTCTGT 2295

RESULT 2
US-09-938-842A-833
Sequence 833. Application US/09938842A
Patent No. US2002160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SAME, AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 833
LENGTH: 2280
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-833

Alignment Scores:
Pred. No.: 0 Length: 2280
Score: 3480.00 Matches: 607
Percent Similarity: 90.7% Conservative: 77
Best Local Similarity: 80.5% Mismatches: 70
Query Match: 83.9% Indels: 0
DB: 3 Gaps: 0

US-09-419-679-6 (1-757) x US-09-938-842A-833 (1-2280)
Qy      1  MetTTPrLeuLeuYsrPheAlaGluGlyAerProTPrLeuAerGlnIleAerAerHis 20
Db      1  ATGTGAACTGAAGATCGCGAAGAGGTAGTCAAGGCTTAGAACACCAATTAATCAC 60
Qy      21  ValGlyAerGlnValTPGluPheAerProLeuLeuGlySerProGlnAerLeuGln 40
Db      61  GTGGGAAGACAGTTTGGAGTTGATCCGAATCTCGTATCTCTGAGATCTCCGCC 120
Qy      41  IleGluValAerGlnAerPheHisAerAerAerGlnPheThiAerValHisAerAlaAer 60
Db      121  GTGGAAGAGCTAGAGAGTCTTTTCCGATATGATTCGTCGAGAAACATAGGCCGAT 180
Qy      61  LeuLeuMetAerMetGlnPheAlaAerGluAerProThiAerGluValLeuProLeuVal 80
Db      181  CTGCTTATGGCGCTTCAGTTTCAAGAGAAATTTGATTAGCCAGTTTACCTCAAGTC 240
Qy      81  GlyValAerAerIleGluAerValThiGlnGluIleValThiAerThiLeuAerArgAla 100

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Db      241  AAAATCAAGACACATGATGATGTTACAGAGAGATGTGGAACACCGTTAAAGAGGGGT 300
Qy      101  ValSerPheHisSerThiLeuGlnCysHisAerGlyHisTPPrProGlyAerPtyGly 120
Db      301  CTAGATTCTTATTCAACTTATACAGGCACACACAGGGCCATGGCCAGAGATTATAGTGGT 360
Qy      121  ProMetPheLeuMetProGlyLeuValIleThiLeuSerIleThiGlyAlaLeuAerHis 140
Db      361  CCTATGTTCTTCTCCAGAGCTGATTAATTAACCTTCCATTAATCGAGACATGAAATCA 420
Qy      141  ValLeuThiGlnGluHisAerGlyLeuIleCysAerGlyLeuTyrlAerHisGlnAerHis 160
Db      421  GTATTGTGGAAACAATTAACAAAGAAATGGCGGTTATCTCTAATACACAGAAATGAG 480
Qy      161  AerGlyGlyTPPrGlyLeuHisIleGluGlyProSerThiMetPheGlySerValLeuSer 180
Db      481  GACGGAGGTTGGGGTTTACATATTGAGGGCCCTAGCACCATGTTGGGTCTGTGTGAAC 540
Qy      181  TyrlIleThiLeuAerGluLeuGlyGluIlyProAerAerGlyGlnGlyLeuMetGlyHis 200
Db      541  TATGTTACTTAAGGTGCTTGGAGAGACCTTAACGATGAGATGAGATATGGAGAAA 600
Qy      201  AlaAerAerTPPrIleLeuGlyHisIleGlyAlaThiTyrlIleThiSerTPPrGlyHisMet 220
Db      601  GCACGAGACTGTGATCTTAATCATATGCTGTCTACCAATATTACATCTTTGGGGGAAAAATG 660
Qy      221  TPPrLeuSerValLeuGlyValTyrlGluTPSerGlyAerAerProLeuProGluIle 240
Db      661  TGGCTATGGGATCTTGGAGCTTTGAAATGCTCGGAAATTAACCCATCGCACCTAGATA 720
Qy      241  TPPrLeuLeuProTyrlMetLeuProPheHisTPPrGlyAerMetTPPrCysHisCysAerMet 260
Db      721  TGGCTTCTCCCATATTTCTGCAATATACATCCAGAGAGATGTGGATGTGATGTGAAAG 780
Qy      261  ValTyrlLeuProMetSerTyrlLeuTyrlGlyAerPheValGlyProIleSerProThi 280
Db      781  GTGTATCTGCCAATGTCGATTTGATTTGAGAAAAGTTTGGGTGCCATTAACGTCCACT 840
Qy      281  ValLeuSerLeuAerGlySerGlyLeuTyrlThiValProTyrlHisAerPheAerTPPrAerGln 300
Db      841  GTTTTATCATCTAGAAAGAGGCTTTTCAAGTACATATCATGATGATCAATCGAATGAA 900
Qy      301  AlaAerAerLeuCysAlaAerGlyAerLeuTyrlTyrlProHisAerProLeuValGlnAerIle 320
Db      901  GCACGCAACCTTGGCGCAAGAGAGATTATCTACCCCATCCACTGTTGCAAGATATT 960
Qy      321  LeuTPPrAlaSerLeuHisAerPheLeuGluTPPrIleLeuMetHisTPPrProGlyHisArg 340
Db      961  CTTTGGGCACTCACTTCAATAAGATTTGTTGAGCCTGTTCTGATGCAATGGCTGTGGTAAT 1020
Qy      341  LeuAerGlyValAlaIleIleSerAlaLeuGluHisIleHisTyrlGlyAerPheGluAerHis 360
Db      1021  TTGAGGAAAAGGCTTATTAAGAACCGCAATGAACATATTCATTATGAATGAAATATCT 1080
Qy      361  ArgTyrlIleCysAlaIleProValAerHisValLeuAerMetLeuCysSerTPPrValGlu 380
Db      1081  AGGTATCATCTGCAATAGTCCCGTGAAACAAGATTAATAATGCTTGGTGGGTGAGAA 1140
Qy      381  AerProAerSerGlyAlaAerLeuValAerLeuHisIleAerProAerGlyHisAerPheTyrlIle 400
Db      1141  GACCCAAATCAAGAGGCTTCAAGTTGACATTCACATTAAGATTCATTAATCTCTGTGTA 1200
Qy      401  AlaGluAerPheTyrlMetLeuMetGlnGlyTyrlAerGlySerGlnIleTPPrAerThiAlaPhe 420
Db      1201  GCTGAAGATGAGATGAAGATGACAGGTTTATTAACGAAACCAAGTATGAGATACAGGTTT 1260
Qy      421  AlaValGlnAlaIleIleAlaSerAerLeuIleGluGluPheGlyProThiIleAerGlyHis 440
Db      1261  GTATTCAAGCCATTTTGGCACTAATCTGTCGAAAGAAATATGAGGCCCTTTTGGAAAAA 1320
Qy      441  AlaHisThiTyrlIleAerAerSerGlnValLeuGluAerCysAerProGlyAerPheAerHis 460

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QY 241 TTPLeuLeuProTyMeLeuLeuProPheH1SPROG1YAqMeTTPCySH1SCyAaArgMet 260
Db 721 TGGCTTCCCAATATTTCTGCCAATACATCCAGAAAGATGTGGTCATTTGGTAATG 780
QY 261 VAlTYrLeuProMetSerTyTleuTYrGlyLybAArgPheValGlyProIleSerProHr 280
Db 781 GTGTCTTGGCCATGTCTGATTTGTATGGAAAAAGTTTGGGTCCTCAAAAGTCCACT 840
QY 281 VAlleuSerLeuAArgLybGlyLeuTYrTYrValProTyH1aSP1leAerTPaSPgin 300
Db 841 GTTTATACCTAGAAAGAGCTTTTCAACATACATACATCAAGTCACTCACTGCAAGATGA 900
QY 301 A1AaArgAenLeuCyAa1AlybGlybAerLeuTYrTYrProH1aSP1leuValGlnAerIle 320
Db 901 GCAACCAACTTTGGCCAAAGAGATTTATATACCCATCCATCCATCTTGCAAGATAT 960
QY 321 LeuTPAlaSerLeuH1bLybPheLeuGlyProIleLeuMetH1eTPProGlyLybArg 340
Db 961 CTTTGGGCATCACTTCATAGATGTGTAGCCCTGTGTATGCGATGCGCTGGTCAAA 1020
QY 341 LeuAArgLybLybA1a1e1Ser1A1euglyH1a1e1e1TYrGlybAerGlybAerHr 360
Db 1021 TTGAAGAAAGAGCTATAGAAACCGCAATAGAAATATTCATTTATAGATGAATGACT 1080
QY 361 AArgTYrIleCyA11eGlyProValAenLybValLeuAenMetLeuCyAcyTPValGly 380
Db 1081 AGGTACATCTGCATAGTCCCGTGAACAAAGTATTAATATGCTTGTGGTGGTGA 1140
QY 381 AARProAenSerGlybA1aPheLybLeuH1bLeuProArgIleTYrAerTYrLeuTPle 400
Db 1141 GACCCAACTCAGAGGCTTCAAGTTGCACTTACCAAGAAATCATACATTTCTCGGTA 1200
QY 401 A1aGlybAerGlyMeTyMeSerGlnGlyTYrAenGlySerGlnLeuTPaSP1rA1aPhe 420
Db 1201 GCTGAAGATGAATGAAAGATGAGGCTTATACGAAAGCCAGCTTATGAGTACAGCTTT 1260
QY 421 A1AaValGlnA1a1e1leA1aSerAenLeu1eGlybGlybPheGlyProHrIleAArgLyb 440
Db 1261 GCTATTCAGACATTTTGGCACTAACCTGCTGAAGAAATATGGCCCGTTTGA 1320
QY 441 A1aH1eHrTYrIleLybAenSerGlnValLeuGlybAerCyAerProGlybAerLeuAenLyb 460
Db 1321 GCACATTCATTTGTCAAGAAATCCCAAGTGTGAAGACCTCGAGATTCGAATTC 1380
QY 461 TTPTYrAArgH1a1e1SerLybGlyA1aTPProPheSerHrGlybAerH1aSP1aSP1Pro 480
Db 1381 TGGTATCGCCACATTTCTTAAAGGCGCTTGGCTTTCACATGCAAGTCACGGTGGCC 1440
QY 481 I1eSerAerCyAerHrA1aGlybGlyLeuLybA1aValLeuLeuSerLyb1eA1aPro 500
Db 1441 ATCTTCATGCTGCAACCGCAAGAGATGAAAGTCTTGTGCTATCCAAAGTTCCCAAG 1500
QY 501 GlnI1eValGlybProIleAerValLybAerLeuTYrAerSerValAenValIleLeu 520
Db 1501 GCGATTTGTGTGAACCAATAGATGCAAAACGGTATATAGACCTGTATATGTTATCAT 1560
QY 521 SerLeuGlnAenGlybAerGlybPheA1aThrTYrGlybLeuLybAerSerTYrAenTP 540
Db 1561 TCTTTACGAATGCAATGAGGCTTGCACACATATAGCTCACCGGTCAACCCCTGG 1620
QY 541 LeuGlybIle1eAenProA1aGlybThrPheGlybAerIleValIleAerTYrProTYrVal 560
Db 1621 TTGAAGCTATACAAACCGCAAGAACTTTGGCAATTTGTATATGTTATCTTACGTG 1680
QY 561 GlnCyAerThSerA1aA1a1eGlnA1aLeuA1aSerPheAerGlybLeuTYrProGlyH1a 580
Db 1681 GAATGTACATCAGTGTCTATCCAAAGCTTGTATATCATTTGCAAGCGTATCCGTGAT 1740
QY 581 AArgAerGlybGlybIleGlnH1aCyA1aAerLybA1aHrThrPheIleGlybLybIleGln 600
Db 1741 CGAAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800

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QY 601 A1aSerAerGlySerTPTyGlySerTPGlyValCySPeHrTYrGlyA1aTPPhe 620
Db 1801 GAGCAGATGGCTCATGATAGATCATGGGCTGTTCCTTCACGTATAGTACGTGTT 1860
QY 621 G1yValLybGlyLeu1eA1aGlyAArgSerPheSerAenCySerSerIleAArgLyb 640
Db 1861 GAGTGAAGAGGCTGTGTGTGTGCAAAAACATGAAAACCTCCACATGTGCTAAA 1920
QY 641 A1aCyGlybPheLeuLeuSerLybGlybLeuProSerGlybGlyTPPGLyGlySerTyLeu 660
Db 1921 GCTTGTGATTTCTATTTGTGAAACAAACCTTGGCGGCTGGGAGAAAGCTATCT 1980
QY 661 SerCyGlnAenLybValTYrSerAenLeuGlybA1aAArgSerH1aValA1aerHr 680
Db 1981 TCATGCAAGACAGCTCTATTCAAACCTTATAGGCAACAGATCTCAGCTGTGAATCA 2040
QY 681 G1yTPAlaMeTyMeLeuA1eul1eAerA1aGlybA1aLybAArgAerSerGlnProLeu 700
Db 2041 GCATGGGCTATGCTGCACCTCATTTGTGTGTGGCAAGCTGAGTACCGGAAACCACTA 2100
QY 701 H1aArgA1aA1aTYrLeu1leAenSerGlnLeuGlybAerGlybAerProGlnGln 720
Db 2101 CACCGGCTGCAAGATCTTGTATATGCTCAAAATGAGAAATGATTTTCACAAACG 2160
QY 721 GlnI1eMerGlybValPheAenLybAenCyMeT1eHrTYrA1aA1aTYrAArgAenIle 740
Db 2161 GAATTAATGGAGCTTTCATATAGAACTGCATGATTAATATGCGCGGTATGAAACAT 2220
QY 741 PheProIleTPAlaLeuGlybGlybGlybGlybGlybGlybGlybGlybGlybGlyb 754
Db 2221 TTTCCGATATGGGCTTTGGGGAGATACGCTTTCAGATTTA 2262

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RESULT 4
US-10-425-115-91064
; Sequence 91064, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5322)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 91064
; LENGTH: 2776
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_183051C.1
US-10-425-115-91064

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Alignment Scores:
Pred. No.: 0 Length: 2776
Score: 3248.00 Matches: 575
Percent Similarity: 86.8% Conservative: 80
Best Local Similarity: 76.2% Mismatches: 96
Query Match: 78.3% Indels: 4
DB: 9 Gaps: 2

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US-09-419-679-6 (1-757) x US-10-425-115-91064 (1-2776)

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QY 1 MetTPLybLeuLybPheA1aGly---GlyGlyAenProTPLeuAArgThLeuAenAen 19
Db 202 ATGTGGCGCTGTGAGATCGGAGGGGGGGGACCCCTGGCTCCGACGAAGAACGCC 261
QY 20 H1eValGlyAArgGlnValTPGlybPheAerProLybLeuGlySerProGlnAerLeu 39
Db 262 CAGCTGGCGCGCAAGGTCTGGAGTTGCAC-----GCTCCGCCGACCCGACCC 312

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QY 40 GluIleGluValArgGlnAsnPheHisAspAsnArgPheThrHisLeuHisSerVala 59
 Db 313 GCCGCGACGGCGCGCGCGCTTGGCCGGCAGACAGGGCCACTGAACACAGCGCC 372
 QY 60 AspleuLeuMetArgMetGlnPheAlaArgGlnAsnProThrArgGlnValLeuProLys 79
 Db 373 GACCTCCCTCAAGCCGATCCAGTTCGCCAAGAAATCTCTTGAGCTTGACCTTCAGCCG 432
 QY 80 ValGlnValLysAspValIleThrGlnGluIleValThrLysThrLeuAspArg 99
 Db 433 ATCAAGCTCGGTGACACAGAAAGACCTAACCGAGAGCGGTGTCTACTACTTGAAGAG 492
 QY 100 AlaValSerPheHisSerThrLeuGlnCysHisAspGlnHisIleProGlnYAspTyrGly 119
 Db 493 GCATTCAGCCGCTTTCTACTCTCCAGGCACATATGAGACACTGGCCGTGGGGATTATGGT 552
 QY 120 GlnProMetPheLeuMetProGlnLeuValIleThrLeuSerIleThrGlnAlaLeuAsn 139
 Db 553 GGCCCTATGTTCTTATGCCAGGCTTGATCATTAACATGTATGTAGACTGGAGCACTAAGC 612
 QY 140 ThrValLeuThrGlnGluHisArgGlyLeuIleCysAspGlyTyrLeuTyrAsnHisGlnAsn 159
 Db 613 ACTGCTGTGATCATGAAGACACAGAAAGAGATCGGTGGATCTTTATATATCATCAGAT 672
 QY 160 LysAspGlyGlyTyrGlyLeuHisIleGlnGlyProSerThrMetPheGlySerValLeu 179
 Db 673 GAAGATGGTGGCTGGGGCTTGACATTTGAGGGTCCAAACACATGTTTGGTCCAGCACTG 732
 QY 180 SerTyrIleThrLeuArgLeuLeuGlnGlyGlnProAsnAspGlyGlnGlyGlnMetGln 199
 Db 733 ACCTAACGTACTTGTAGATGCTTGGAGAGGAGACACAGATAGTGAGATGGAGCAATGAG 792
 QY 200 LysAlaArgAspTyrIleLeuGlnHisIleGlnGlyAlaThrTyrIleThrSerTyrGlyLys 219
 Db 793 AAAGGCCAACTGGATCTTAGACCATGGCGAGACATATATATACACTTGGGGAGAG 852
 QY 220 MetTyrLeuSerValLeuGlnValTyrGlnTyrSerGlyAsnAsnProLeuProGln 239
 Db 853 TTTTGGGCTCTGGATCTTGGTGTATTTGAATGGTGTGTAACAAACCGGTACACCGAGAA 912
 QY 240 IleTyrLeuLeuProTyrMetLeuProPheHisIleProGlnArgMetTyrCysAlaArg 259
 Db 913 GTATGGCTACTGCATATCTCTGCATTCACCCAGAGAGATGTGGTGCATTTGTCGA 972
 QY 260 MetAlaTyrLeuProMetSerTyrLeuTyrGlnLysAspPheValGlnProIleSerPro 279
 Db 973 ATGGGTATTTGCCAATGTGTACATCTATGAGAAAGAGTTTGTGGTGAATACACCA 1032
 QY 280 ThrValLeuSerLeuArgGlnLeuTyrThrValProTyrHisAspIleAspTyrAsp 299
 Db 1033 CTCGTGTGGAAATTAGAAAGAACTTTCAAGACCTTACAGCAAGATTGATTGGGAC 1092
 QY 300 GlnAlaArgAsnLeuCysAlaLeuGlnAspLeuTyrTyrProHisIleProLeuValGlnAsp 319
 Db 1093 AAGGCCCGCATCTATGTGCTAAGAGAGATCTGATCATCCACTTCATTTGTTCAAGAT 1152
 QY 320 IleLeuTyrAlaSerLeuHisIleLysPheLeuGlnProIleLeuMetHisIleTyrProGlyLys 339
 Db 1153 GCTCTATAGGCGCACTCTCCATTAATTTGTGAACCAAGTATGATGAGTTGGCTGGGCACT 1212
 QY 340 ArgLeuArgGlnLysAlaIleIleSerAlaLeuGlnHisIleHisTyrGlnAlaAspGlnAsn 359
 Db 1213 AAATTGAGGAGAAAGCTCTGGAGACACACCTGACACATGTCTCATGAGAGTAGAGAAC 1272
 QY 360 ThrArgTyrIleCysIleGlyProValAlaAsnLysValLeuAsnMetLeuCysCysTyrVal 379
 Db 1273 ACTGGGTACATTTGCTATGTGCTGTAAACAAGGATTAATATGCTTGTGCTGGAGTT 1332
 QY 380 GlnAspProAsnSerGlnAlaPheLysLeuHisIleLeuProAlaGlyIleTyrAspTyrLeuTyr 399
 Db 1333 GAAGATCCAAACTAGAGGCGCTTCAAACTCCACACAGCTATGACTACTTGTGG 1392
 QY 400 IleAlaGlnAspGlyMetLysMetGlnGlyTyrAsnGlySerGlnLeuTyrAspThrAla 419

Db 1393 :: 1452
 CTTGCTGAAGATGGCAGTAAGATGCAGGCTATATAGTAGCCAACTTGGGATACAGCT
 QY 420 PheAlaValGlnAlaIleIleHisAspAsnLeuIleGlnGlnPheGlyProThrIleArg 439
 Db 1453 TTTCAATGTTCAAGCATTTGTGGCTTACCAACCTTACCGAAAGAGTTTGTGTCCACCTTTAA 1512
 QY 440 LysAlaHisThrTyrIleLysAsnSerGlnValLeuGlnAspCysProGlnYAspLeuAsn 459
 Db 1513 CTAGACACAACTATATCAAGAAATCACAGTTCTTACAGACTGCCCTGGGATCTGAT 1572
 QY 460 LysTyrTyrArgHisIleSerLysGlyAlaIleTyrProPheSerThrGlnYAspHisGlyTyr 479
 Db 1573 GACTGTACGCCCAACATCATTAAGGGCGATGGCCATTTCAACCGGGATCATGTTGG 1632
 QY 480 ProIleSerAspCysThrAlaGlnGlyLeuLysAlaValLeuLeuLeuSerLysIleAla 499
 Db 1633 CCTATATCTATGTGACCTGCTGAAGACTAAAGCTTCATTAATTTGTTATCAAAAGATTTCT 1692
 QY 500 ProGlnIleValGlnGlyProIleAspValLysArgLeuTyrAspSerValAsnValIle 519
 Db 1693 CTTGAATTTGTGGTGGACCGGATGAAGCTAATATGATTTATATGATGCTGCAGTTGCTG 1752
 QY 520 LeuSerLeuGlnAsnGlyLysPheAlaThrTyrGlnLeuLysArgSerTyrAsn 539
 Db 1753 ATGCTTATATGATATGATATGATGTTGTGGCTTATATGAACTCAACAGATCCTATGCC 1812
 QY 540 TyrLeuGlnIleIleAsnProAlaGlnThrPheGlyAspIleValIleAspTyrProTyr 559
 Db 1813 TGGCTGAGGTGATCAATCTGCTGAGACCTTTGGGATATTTGATGTGATTAACCGTAT 1872
 QY 560 ValGlnCysThrSerAlaAlaIleGlnAlaLeuAlaSerPheArgLysLeuTyrProGly 579
 Db 1873 GTTGAATGTATCATCAGACGATATCCAGCCCTGACATCATTCAGAAACTATACCTCTGGG 1932
 QY 580 HisArgArgGlnGlnIleGlnHisCysIleAspLysAlaThrThrPheIleGlnLysIle 599
 Db 1933 CACCGCAGAAAGAGTGAACAATCTGATCAGAAAGCTGCTATTCATTGAGAGATTT 1992
 QY 600 GlnAlaSerAspGlySerTyrTyrGlySerTyrGlyValCysPheThrTyrGlyAlaTyr 619
 Db 1993 CAGAAAGTACCGTTCATGATGTGGCTCTGGGCTGTGGTTCACAGTACGGGCACTTGG 2052
 QY 620 PheGlyValLysGlyLeuIleAlaGlyArgSerPheSerAsnCysSerSerIleArg 639
 Db 2053 TTTGGTGTGAAGGACTATATCTGCTGCTGTGAACATTTGAGACAGCTCCGCAATCAGA 2112
 QY 640 LysAlaCysGlnPheLeuLeuSerLysGlnLeuProSerGlyGlyTyrGlyGlnSerTyr 659
 Db 2113 AAGGCATGGCGCTTCTGTATCAAAAGACCTTCCGCTGGCTGGGAGAAAGCTAT 2172
 QY 660 LeuSerCysGlnAsnLysValTyrSerAsnLeuGlnGlyAsnArgSerHisValAlaAsn 679
 Db 2173 TTATCGCTCAAAACCGGTTTACCAACATCTAAAGGCAACGAGCTTCAGCGCAAC 2232
 QY 680 ThrGlyTyrAlaMetLeuAlaLeuIleAspAlaGlyGlnAlaLysArgAspSerGlnPro 699
 Db 2233 ACTGGTTGGGCACTGCTGGCGCTGATTTGATGCAGAGACGCCAGAGATATCCGCGCCT 2292
 QY 700 LeuHisArgAlaAlaAlaTyrLeuIleAsnSerGlnLeuGlnAspGlyAspPheProGln 719
 Db 2293 CTACACGACACAGACGAGCGTTTGTATTAATCTTGCAAGTCAAGAGCGAGAAATTTCCACAG 2352
 QY 720 GlnGlnIleMetGlyValPheAsnLysAsnCysMetIleThrTyrAlaAlaTyrArgAsn 739
 Db 2353 CAAGAGATCATAGAGAGTTCACAAGAACTGCATGTCTGTTATCTCCAGTACAGAGAAC 2412
 QY 740 IlePheProIleThrAlaLeuGlnGlyTyrGlnSerGlnValLeu 754
 Db 2413 ACCTTCCGATGTGGGCTTGGAGAGATACCGGTGCCGAGTCTCTG 2457

RESULT 5
 US-10-437-963-71137

Alignment Scores:	
Pred. No.:	0
Score:	3240.50
Percent Similarity:	87.1%
Best Local Similarity:	74.9%
Query Match:	78.1%
B:	8
Length:	4120
Matches:	564
Conservative:	92
Mismatches:	96
Indels:	1
Gaps:	1

2000 *Environ Biol Fish* 58:381–391

Db	1082	TATATTGATGTGGTCCAGTAACAAGGATTAATTAATGCTGTGGCTGGATTAAGACT	1144
Qy	382	ProaenSerGluAlaPheIysLeuHisLeuProAlaGlyLeuTyrAspTyrLeuTrpIleAla	401
Db	1142	CCAAACTCAGAGGCAATTCMAATCCACATTCGAAAGTCCACAGATTACCTTAGATGTGCA	1201
Qy	402	GluAspGlyMetLeuMetGlnGlyTyrAsnGlySerGlnLeuTrpAspThrAlaPheAla	421
Db	1202	GAAGATGGCATAAAAATGACAGGGTTATATATGGAAACCGAGCTGTGGACACACTTTCACA	1261
Qy	422	ValGlnAlaIleIleAlaSerAsnLeuIleGluGluPheGlyProThrIleArgIysAla	441
Db	1262	GTTCAAGCATATAGTGGCTTACTGGCTCATTTGAAGATTGGTCTTACTTAACTAGCA	1321
Qy	442	HisThrTyrIleIysAsnSerGlnValLeuGluAspCysProGlyAspLeuAsnIleTyr	461
Db	1322	CATGGCTATATAAAGAAAAGCAGGGTTATTCATATGCATGACTGCCCTGGAGATTTTAGTCAGTGG	1381
Qy	462	TyrArgHisIleSerIysGlyAlaTrpProPheSerThrGlyAspHisGlyTrpProIle	481
Db	1382	TACCCGCACATATCTTAAAGTGTGACATGGCCCTTTCTACTCGCGATCATGGTTGGCCTATA	1441
Qy	482	SerAspCysThrAlaGluGlyLeuIysAlaValLeuLeuLeuSerIysIleAlaProGlu	501
Db	1442	TGAGATTGCACTGSCAGAAAGACTTAAGGCGGCAATTATTCATTCGAAGATTCTCCAGACT	1501
Qy	502	IleValGlyGluProIleAspValIysValArgLeuTyrAspSerValAsnValIleLeuSer	521
Db	1502	ATTGTGGCGAAGCAGGTGAAGATTATATAGACTGATGATTCGTGTCAAATTGGTGAAGTCA	1561
Qy	522	LeuGlnAsnGlyAspGlyGlyPheAlaTrpTyrGluLeuIlyArgSerTyrAsnTrpLeu	541
Db	1562	TTCATCAATAGATATATGGTGGATTTGCAACATATGAACCTACAAGGCTTATAGCCTGGCTG	1621
Qy	542	GluIleIleAsnProAlaGluThrPheGlyAspIleValIleAspTyrProTyrValGlu	561
Db	1622	GACCTATATCATCTCTGTAGACCTTTGGGACATTTGTATGATTATTCCTTATGTGGAA	1681

QY 562 CyeThrsrAlaAlaIleGlnAlaLeuAlaSerPheArglyLeuTyPProGlyHHisArg 581
Db 1662 TGCACCTTACGACGATTCAGGCGCTTGACACGATTTAAAGACTTACCCTGGACACCGC 1741
QY 582 ArgGluGluIleGlnHisCyeIleAspValaThrThrPheIleGluLeuIleGlnAla 601
Db 1742 AAGAGTAAATAGACACTGTATAGCAAAAGCTGTACTATTATAGAGGATATCAAAA 1801
QY 602 SerAspGlySerTrpTyGlySerTrpGlyValaCysPheThrTyGlyAlaTrpPheGly 621
Db 1802 AGCGATGCTTCAGTATGATGCTTCGGCGCTGTTTGTATTACCTATAGGACATGGTTTGT 1861
QY 622 VallyAspGlyLeuIleAlaAlaGlyArgSerPheSerAsnGlySerSerIleAspVala 641
Db 1862 GTAAAGGAGATTAATGCTGCTGGTAGACATTCAAAACAGCTCCGATCAAGAAAGCA 1921
QY 642 CysGluPheLeuLeuSerIleGlnLeuPProSerGlyTyTrpGlyGlySerTyPLeuSer 661
Db 1922 TGTGACTTTTCTTCTCAAAAGAGCTTCCTTCTGAGGCTGGGAGAAAGCTATTGTCA 1981
QY 662 CysGlnAsnLysValTyPSerAsnLeuGlyLysAsnArgSerHisValaIleAsnThrGly 681
Db 1982 TCCCAAGATCAGGTTTATATCCATCTCGAAGGGAAGCACTCATGCGGTGAACACTGT 2041
QY 682 TrpAlaMetLeuAlaLeuIleAspAlaGlyGlnAlaLysArgAspSerGlnProLeuHis 701
Db 2042 TGGGCGCATGCTAGCCCTTATCGATCGAGGCGAGCTGAGAGAGATCCAAATTCCTTTCAT 2101
QY 702 ArgAlaAlaAlaTyPLeuIleAsnSerGlnLeuGlyAspGlyAspPheProGlnGlnGlu 721
Db 2102 CGAGCAGCGAAGCTTTTATATCACTTACATCGGAAGATGTGATTTCCCGAGAAAG 2161
QY 722 IleMetGlyValaPheAsnLysAsnGlySerMetIleThrTyPAlaAlaTyPArgAsnIlePhe 741
Db 2162 ATCATTTGAGTCTTCAACAAAACATGATGATCACTACTCCGAGTATAGAAACATCTTC 2221
QY 742 ProIleTrpAlaLeuGlyGlyTyPTrpGlnSerGlnValaLeu 754
Db 2222 CCTATTGGGCGCTTGGGAGTACGTCGCGGCTTCGTG 2260

RESULT 6
US-10-425-114-25096
; Sequence 25096, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10-425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 25096
; LENGTH: 2638
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3689-250-D7_PL1
US-10-425-114-25096

Alignment Scores:

Pred. No.: 0 Length: 2638
Score: 3237.00 Matches: 571
Percent Similarity: 86.8% Conservative: 84
Best Local Similarity: 75.6% Mismatches: 96
Query Match: 78.0% Indels: 4
Gaps: 3

US-09-419-679-6 (1-757) x US-10-425-114-25096 (1-2638)
QY 1 MetTrpLysLeuLysPheIleAlaGlu--GlyGlyAsnProTrpLeuArgThrLeuAsn 19
Db 198 ATGTGGGCGGCTCGGATCGGAGAGGGGGGAGCCCTTGCTTACACACAAAGAGCC 257
QY 20 HisValGlyArgGlnValaTrpGluPheAspProLysLeuGlySerProGlnAspLeu 39
Db 258 CACCTCCGCGCCAGAGGTGGAGTTGAC---GCCCGCGGACCCCGAGCC----- 308
QY 40 GluIleGlyValaArgGlnAsnPheIleAspAsnArgPheThrHisLysHisSerAla 59
Db 309 GCGCTGACGCGCGCGCGCGCTGCTGCGCCACAGAGGCGCCACTCAAGCAGAGCGCC 368
QY 60 AspLeuLeuMetAspMetGlnPheAlaArgGlnAsnProThrArgGlyValaLeuProLys 79
Db 369 GACCTCTCATGCGCCATCCAGTTGCGCAAGAAACCTGATGAGCTTCACCTTCCAGGC 428
QY 80 ValGlyValaLysAspIleGlnAspValaThrGlnGluIleValaThrLysThrLeuArgArg 99
Db 429 ATCAAGCTCGGTGACATGAAGATGTGACCGAGAACTGTGTGACTACATTAAGAG 488
QY 100 AlaValSerPheHisSerThrLeuGlnCysHisAspGlyHisTrpProGlyAspTyGly 119
Db 489 GCATTCAGCGGTTCTCTACTCTCCAGGACATGATGAGACACTGGCGTGGGATTTATGT 548
QY 120 GlyPheMetPheLeuMetProGlyLeuValaIleThrLeuSerIleThrGlyAlaLeuAsn 139
Db 549 GGTCTTATGTTCTTATGCGAGGCTTATCAATTAATGTATGACTGGAGCACTAAAC 608
QY 140 ThrValLeuThrGlnGluHisArgLysGluIleCysArgTyPLeuTyPAsnHisGlnAsn 159
Db 609 ACTGTCTTGATTCATGAAACACAGAGAGATCCGCGGATCTTTATATACACAGAT 668
QY 160 LysAspGlyGlyTyPTrpGlyLeuHisIleGlnGlyProSerThrMetPheGlySerValLeu 179
Db 669 GAAGATGGCGGCTGGGCTTGCAATGAGGCTCAAGACACATGTTGCGCTCAGACACTG 728
QY 180 SerTyPTrpLeuAspGlyLeuGlyGlyGluTyPProAsnAspGlyGlnGlyGluMetGlu 199
Db 729 ACCATGTATTTTGAATGCTTGGAGAGGACCAATGATGAGATGAGCCATGGAG 788
QY 200 LysAlaArgAspTrpIleLeuGlyHisGlyGlyValaThrTyPTrpIleThrSerTrpGlyLys 219
Db 789 AAGGTGGAATCTGATTTAGACATGTGAGACACATATATACATCTGGGGAG 848
QY 220 MetTrpLeuSerValLeuGlyValaTyPTrpSerGlyAsnAsnProLeuProGlu 239
Db 849 TTTTGGCTTTCGATACATAGGTGATTTGAATGCTGTGATCAACCCGCTGCCACAGAA 908
QY 240 IleTrpLeuLeuProTyPTrpMetLeuProPheHisAspProGlyAspMetTrpCysHisCysArg 259
Db 909 GTATGGCTACAGCCATATCTCTCCATTTCAACCGAGAGAGATGTGTGTCTGTGCA 968
QY 260 MetValTyPLeuProMetSerTyPLeuTyPTrpLysArgPheValaGlyProIleSerPro 279
Db 969 ATGGTGTATTTTGCATATGTCTATCTTATGGAGAGGTTTGTGGCCGAATACACCA 1028
QY 280 ThrValLeuSerLeuArgLysGlyLeuTyPThrValaProTyPHisAspIleAspTrpAsp 299
Db 1029 CTTGCTTGGAATTAAGAGAGAACTTTCAAAAGACCTTACAGCAAGATGATGGGAC 1088
QY 300 GlnAlaArgAsnLeuCysAlaLysGlyAspLeuTyPTrpProHisAspProLeuValaGlnAsp 319
Db 1089 AAGGCGCGTAACTATGTCGCAAGAGATCTGTATCAACCAACCAATTCCTTCATAT 1148
QY 320 IleLeuTrpAlaSerLeuHisLysPheLeuGluProIleLeuMetHisTrpProGlyLys 339
Db 1149 GTGTATAGGCGCACTTCATTAATTCGTATACCAAGTATGATGATTCGCTGGCAGC 1208
QY 340 ArgLeuArgGlyLysAlaIleIleSerAlaLeuGlnHisIleHisTyPTrpGlyAspGluAsn 359

Db 1209 AAATTAGGAGAAAGCTCTGGAAACAGTCATGCAACATGTTTATTATGAGATGAGAAC 1268
Qy 360 ThrArgTyrIleCysIleGlyProValAsnLysValLeuAsnMetLeuCysCysTrpVal 379
Db 1269 ACTGCTTATATTTGGCATTTGCTCTGTAAACAGATGATTGATATGCTTGTGCTGAGATT 1328
Qy 380 GluAspProAsnSerGluAlaPheLysLeuHisLeuProArgIleTyrAspTyrLeuTrp 399
Db 1329 GAAAGATCCAAATCCGAGAGCTTCAAACTTCATATCCCAAGGTCTATGATTAATTCGTGG 1388
Qy 400 IleAlaGluAspGlyMetLysMetGlnGlyTyrAsnGlySerGluLeuTrpAspThrAla 419
Db 1389 CTTCGTAAGATGCGCATGAAAGATGCGGATATATATGCGACCACTTTGGATACAGCT 1448
Qy 420 PheAlaValAlaGlnAlaIleIleAlaSerAsnLeuIleGluGluPheGlyProThrIleArg 439
Db 1449 TTCACAGTTCAAGCCATTGTGGCTACCAACTTATTGAAGATGGTGTCTCACTCAAA 1508
Qy 440 LysAlaHisThrTyrIleLysAsnSerGlnValLeuGluAspCysProGlyAspLeuAsn 459
Db 1509 CTAGCACACAACTATCAAGAAATTCACAGTTCTTGAGACTGCGCTGTGATCTGAT 1568
Qy 460 LysTrpTyrArgHisIleSerLysGlyAlaTrpProPheSerThrGlyAspHisGlyTrp 479
Db 1569 GACTGTACCGCCACACATCTMAAGGTGATGCGCTTCACATGCTGATCATGAGTGG 1628
Qy 480 ProIleSerAspCysThrAlaGluGlyLeuLysValIleLeuLeuSerLysIleAla 499
Db 1629 CTTATATCTGATTTGCACTGCTGAAAGCATMAAGCCTCATATATGTTATCAAGATCTCT 1688
Qy 500 ProGluIleValGlyLysProIleAspValLysArgLeuTyrAspSerValAsnValIle 519
Db 1689 CCCAAATTTGGTGTGACCGATGAAAGCTAATAGATTATGATCTGCTGAGTTGTCTG 1748
Qy 520 LeuSerLeuGlnAsnGluAspGlyGlyPheAlaThrTyrGluLeuLysArgSerTyrAsn 539
Db 1749 ATGCTTATATGATATATATATGCGGCTTCGCAACATATGAACTCAAGATCTTATCCC 1808
Qy 540 TrpLeuGluIleIleAsnProAlaGluThrPheGlyAspIleValIleAspTyrProTyr 559
Db 1809 TGGTGTAGCTGATCAATCTGCTGAGACTTGGGGATTTGTGATTGATTCACCGTAT 1868
Qy 560 ValGluCysThrSerAlaAlaIleGlnAlaLeuAlaSerPheArgLysLeuTyrProGly 579
Db 1869 GTTGAATGTATCATCAGAGCAATTCAGCCCTGACATCATTTCAAAAATCAATACCTGG 1928
Qy 580 HisArgArgGluGluIleGlnHisCysGlyAspLysAlaThrThrPheIleGluLysIle 599
Db 1929 CACCGCAGAAAGAGGTGATTAATCTGTATCAGCAAAAGCTTCCAAATTTCAATCGAGATAT 1988
Qy 600 GlnAlaSerAspGlySerTyrTyrGlySerTrpGlyValLysPheThrTyrGlyAlaTrp 619
Db 1989 CAAAAAGCATGATGTATGATGCTGCTTGGCCCTTTGTTTACATACGGACCTGG 2048
Qy 620 PheGlyValLysGlyLeuIleAlaAlaGlyArgSerPheSerAsnCysSerIleArg 639
Db 2049 TTTGGTGTGAAGGACATTAATGCTGCTGTGTAAGAACATTTGAGAACAGTCCGTGCAATTA 2108
Qy 640 LysAlaCysGluPheLeuLeuSerLysGlnLeuProSerGlyGlyTyrGlyLysLeuTyr 659
Db 2109 AAGGCATGCACTTCTGTTGTCAAAAGAACTTCCTCCGCTGCTGGGAGAAAGCTAT 2168
Qy 660 LeuSerCysGlnAsnLysValTyrSerAsnLeuGlnLysAsnArgSerHisValValAsn 679
Db 2169 TTGTCACTTCAMAGCCAGGTTTACCAACATTCMAAGCCAAACCGGCTCTATGCACTAAC 2228
Qy 680 ThrGlyTyrAlaMetLeuAlaLeuIleAspAlaGlyGlnAlaLysArgAspSerGlnPro 699
Db 2229 ACTAGTTGGGCGCATGCTGGCTGTATGATGACAGCCAGCCAGAGATCCCAAGCCT 2288
Qy 700 LeuHisArgAlaAlaAlaTyrLeuIleAsnSerGlnLeuGluAspGlyAspPheProGln 719
Db 2289 CTACACCGAGCAGAAAGTTTGTATCAACTTCGAATACATGATGAGAAATTTCTCTAG 2348

Qy 720 GlnGluIleMetGlyValPheAsnLysAsnCysMetIleThrTyrAlaAlaTyrArgAsn 739
Db 2349 CAAGAGATCATGAGAGGTTTCAACAAGAACTGATGATAGCTACTCCCACTACAGAAC 2408
Qy 740 IlePheProIleTrpAlaLeuGlyGlyTyrGlnSerGlnValLeu 754
Db 2409 ATCTTCCGATTTGGGCTCTGGGTGATGATCCGGTGGAGTCTTG 2453
RESULT 7
US-10-425-115-90182
; Sequence 90182, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 90182
; LENGTH: 2786
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_182249C.1
US-10-425-115-90182
Alignment Scores:
Pred. No.: 0 Length: 2786
Score: 3237.00 Matches: 571
Percent Similarity: 86.8% Conservative: 84
Best Local Similarity: 75.6% Mismatches: 96
Query Match: 78.0% Indels: 4
DB: 9 Gaps: 3
US-09-419-679-6 (1-757) x US-10-425-115-90182 (1-2786)
Qy 1 MetTrpLysLeuLysPheAlaGlu---GlyGlyAsnProTrpLeuArgThrLeuAsn 19
Db 198 ATGTGCGCTCGATCGGATTCGGAGGCGGCGGACCTTGCTAGACGAAAGACGCC 257
Qy 20 HisValGlyArgGluValTrpGluPheAspPheLysGlySerProGlnAspLeu 39
Db 258 CACGTGCGCGCAGGTGTGGAGTTCCAGC---GCCGCCGCGACCCGACCC----- 308
Qy 40 GlnIleGluLysAlaArgGlnAsnPheHisAspAsnArgPheThrHisLysHisSerAla 59
Db 309 GCGGTGACGCGCGCGCGCGCGCTTCGTGCGCACAGGAGGCGCACCTCAAGCACAGCGCC 368
Qy 60 AspLeuLeuMetArgMetGlnPheAlaArgGluAsnProThrArgGluValLeuProLys 79
Db 369 GACCTCTCATGTGCGATCCAGTTCGCAAGAAATTCGATGAGCTTCACTTCAGCGC 428
Qy 80 ValGlyValLysAspIleGluAspValThrGlnGluIleValThrLysThrLeuArgArg 99
Db 429 ATCAAGCTCGGTAGATAGATAGTGTACCGAGAAAGCTGTGTGACTACATTGAAAAAG 488
Qy 100 AlaValSerPheHisSerThrLeuGlnCysHisAspGlyHisTrpProGlyAspTyrGly 119
Db 489 GCATAGACCGTTTCTCTACTCTCCAGGACATGATGACACTGCGCTGGGATATATGT 548
Qy 120 GlyPrometPheLeuMetProGlyLeuValIleThrLeuSerIleThrGlyAlaLeuAsn 139
Db 549 GGTCTATGTCTTATGCGCAGGCTTGATCATTAACATTGTATGCTGAGAGCATTAAC 608
Qy 140 ThrValLeuThrGluGluHisArgLysGluIleCysArgTyrLeuTyrAsnHisGlnAsn 159
Db 609 ACTGTCTTGATTTGAAACCAAGAAAGATCCCGGTTATCTTTATATACCGAAT 668

QY 160 LysaapGlyGlyTrpGlyLeuHsiIleGluGlyProSerThrMetPheGlySerValIleu 179
:::|||||
DB 669 GAAGATGGCGGCTGGGGCTTGCACTTGAAGSTCCAAAGCAACATTTGGCGCTACACATCG 728
QY 180 SerTyrIleThrLeuArgLeuGluGlyGluGlyProAsnAspGlyGluGlyIleuMetGlu 199
:::|||||
DB 729 ACCCTATGTTATTTGAGATTGCTTGGAAGAGGAGCCAGATAGTGAGATGAGACCATGAG 788
QY 200 LysaIaargAspTrpIleLeuGlyHsiIleGlyValaThrTyrIleThrSerTrpGlyLys 219
:::|||||
DB 789 AAAGGTCCAACTGGATATTAGACCATGGTGAAGAACATATATTAACATCGGGGGAG 848
QY 220 MetTrpLeuSerValIleGluGlyValTyrGluTrpSerGlyAsnAspProLeuProGlu 239
:::|||||
DB 849 TTTTGGCTTTGGATCTAGGATATTTGATGATGCTGGTAAACACCGGTGACCAAGAA 908
QY 240 IleTrpLeuLeuProTyrMetLeuProPheHsiIleProGlyArgMetTrpCysHsiCysArg 259
:::|||||
DB 909 GTATGGCTACCTGCAATCTCTCCCATTTTCAACGAGGAGAGATGGTGGTCAATTGTGCA 968
QY 260 MetValTyrLeuProMetSerTyrLeuTyrGlyLysArgPheValGlyProIleSerPro 279
:::|||||
DB 969 ATGGGTATTGGCCAAATGCTACATTTATGGAAAGAGTTTGTGGCCGAATCAACCA 1028
QY 280 ThrValLeuSerLeuArgLysGlyLeuTyrThrValProTyrHsiAspIleAspTrpAsp 299
:::|||||
DB 1029 CTTCGTTGGATTTAAGAAAGAACTTTTCAAAAGCCCTTACAGCAAGTTGATTTGGAGAC 1088
QY 300 GlnaIaargAsnLeuCysaIaIysGlyLysPheLeuTyrTyrProHsiProLeuValGlnaP 319
:::|||||
DB 1089 AAGGCCCGTAACCTATGTGCGCAAGAGATCTGTACTAACCCCAACCCATTTGCTCAAGAT 1148
QY 320 IleLeuTrpAlaSerLeuHsiIlyPheLeuGluProIleLeuMetHsiIleTrpGlyLys 339
:::|||||
DB 1149 GTGTATGGGCCCACTCCATTAATTCGTGAACCAATATATCATTTGCTGGCGAC 1208
QY 340 ArgLeuArgGlyLysAlaIleIleSerAlaLeuGluHsiIleHsiTyrGlyLysPheGlu 359
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DB 1209 AAATTGAGGAGAAAGCTCTGAAACAGTCATGCAACATTTCTATTAAGAAATGAGAAC 1268
QY 360 ThrArgTyrIleCysIleGlyProValAsnLysValLeuAsnMetLeuCysSerTrpVal 379
:::|||||
DB 1269 ACTGCTTATTTGATTTGGATTTGCTCTGTAAACAAAGTATGAATATGCTTGGCTGGATT 1328
QY 380 GlnaPProAsnSerGlyAlaPheLysLeuHsiIleuProArgIleTyrAspTyrLeuTrp 399
:::|||||
DB 1329 GAAGATCCAAACTCGAGGCTTCAAACTTCATATCCCAACGATCTATGATTTACTTGTG 1388
QY 400 IleAlaGlyAspGlyMetLysMetGlnGlyTyrAsnGlySerGlnLeuTrpAspThrAla 419
:::|||||
DB 1389 CTTCGTGAAGATGCAATGAAGTGAAGGCTTATTAATGGAGCAACCTTTGGATACACT 1448
QY 420 PheAlaValGlnAlaIleIleAlaSerAsnLeuIleGluGlyPheGlyProThrIleArg 439
:::|||||
DB 1449 TTCAAGTTTCAAGCATTTGGCTGCAACCTTATTAAGAGTTTGGCTTCAACCTTAA 1508
QY 440 LysAlaHsiIleThrTyrIleLysAsnSerGlnValLeuGlyLysPProGlyAspLeuAsn 459
:::|||||
DB 1509 CTAGACACAACTAATATCAAGAAATTCACAGGTTCTTGTGATGCTGCCCTGGATCTGAT 1568
QY 460 LysTrpTyrArgHsiIleSerLysGlyValaTrpProPheSerThrGlyAsnHsiIleTyr 479
:::|||||
DB 1569 GACTGTACCGGCAACATCTTAAGAGTGAAGGCAATTTCAACTGCTGATCATAGGTGG 1628
QY 480 ProIleSerAspCysThrAlaGluGlyLeuLysAlaValLeuLeuLeuSerLysIleAla 499
:::|||||
DB 1629 CCTATATCTGATGCACTGCTGAAGCACTAAAGGCTCATTAATTTTCAAGATCTCT 1688
QY 500 ProGluIleValGlyGluProIleAspValLysArgLeuTyrAspSerValAsnValIle 519
:::|||||
DB 1689 CCCAAATTTGTTGGTGAACCGATGAGACCTAATATGATTTATGATGCTGATGCTGTG 1748

QY 520 LeuSerLeuGlnaGluAspGlyGlyPheAlaThrTyrGluLeuLysArgSerTyrAsn 539
:::|||||
DB 1749 ATGCTTATATGATGATTAATGGCGCTTGCGCAATATGAACTACAAAGATCTTATCCC 1808
QY 540 TrpLeuGluIleIleAsnProAlaGluThrPheGlyAspIleValIleAspTyrProTyr 559
:::|||||
DB 1809 TGGTTGAGCTGATCAATCTCGCTGAGACCTTTGGGATATTTGATGATTTACCCGAT 1868
QY 560 ValGlyCysThrSerAlaAlaIleGlnAlaLeuAlaSerPheArgLysLeuTyrProGly 579
:::|||||
DB 1869 GTTAATGTATACATGACGACATTCAGGCTTGACATCATTTCAAAAACTATACCTGGG 1928
QY 580 HsiArgArgGluGluIleGlnHsiCysIleAspLysAlaThrThrPheIleGlyLysIle 599
:::|||||
DB 1929 CACCGCAAGAAAGGCGATTACTGATATGACAAACCTTCCATTTATGAGAGATTT 1988
QY 600 GlnaIaSerAspGlySerTrpTyrGlySerTrpIleValCysPheThrTyrGlyValaTrp 619
:::|||||
DB 1989 CAGAAAGCGATGCTTATGATGCTGCTGGCCGCTTGTTCACATACGGCATTTGG 2048
QY 620 PheGlyValLysGlyLeuIleAlaIleGlyLysArgSerPheSerAsnCysSerSerIleArg 639
:::|||||
DB 2049 TTTGCTGTGAAGGCACTTAATTTGCTGTGTGAACATTTGAACACAGTCTTGCAATTTGA 2108
QY 640 LysAlaCysGluPheLeuLeuSerLysGlnLeuProSerGlyGlyTyrTrpGlyLysSerTyr 659
:::|||||
DB 2109 AAGGCATCCGACCTTCTGCTGTCTCAAAAGAACTTCTCCGTTGGTGGGAGAAAGCTAT 2168
QY 660 LeuSerCysGlnAsnLysValTyrSerAsnLeuGluGlyAsnArgSerHsiValaAsn 679
:::|||||
DB 2169 TTTGCTATCTCAAGCCAGGTTTACACCAATCTCAAAAGCAACCGGCTCATGCGTGAAC 2228
QY 680 ThrGlyTrpAlaMetLeuAlaLeuIleAspAlaGlyGlnAlaLysArgAspSerGlnPro 699
:::|||||
DB 2229 ACTGTGGGCGCAGCTGGCGCTGATTAATGACAGCGCCGAGAGAAATCAACCGCT 2288
QY 700 LeuHsiArgAlaAlaAlaTyrLeuIleAsnSerGlnLeuGluAspGlyAspPheProGln 719
:::|||||
DB 2289 CTACACCGAGCAGCAAGGTTTGTATCACTTGCAATCACATGATGAGAAATTTCTCAG 2348
QY 720 GlnGluIleMetGlyValaPheAsnLysAsnCysMetIleThrTyrAlaAlaTyrArgAsn 739
:::|||||
DB 2349 CAAGAGATCATAGAGAGTTCACAAAGAACTGCATGATTAAGCTATCCCACTACAGAAC 2408
QY 740 IlePheProIleTrpAlaLeuGlyGlyTyrGlnSerGlnValLeu 754
:::|||||
DB 2409 ATCTTCCGATTTGGGCTCTGGGTGAGTACCGGCGAGCTTGG 2453

RESULT 8
US-10-437-963-71159
; Sequence 71159, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 71159
; LENGTH: 2355
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_7165C.1

US-10-437-963-71159

Alignment Scores:

Pred. No.:	0	Length:	2355
Score:	3234.00	Matches:	566
Percent Similarity:	84.4%	Conservative:	92
Best Local Similarity:	72.6%	Mismatches:	96
Query Match:	78.0%	Indels:	26
DB:	8	Gaps:	2

US-09-419-679-6 (1-757) x US-10-437-963-71159 (1-2355)

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QY 1 MetTPLeuLeuLeuPheAlaGlu---GlyGlyAsnProTTPLeuArgThrLeuAsn 19
DB 1 ATGTGGCGGCTGAGGGTGGCGGAGGCGGGGGGACCCTGGCTGGCGCAGAAACGGC 60
QY 20 HLeValGlyArgGluValTProGluPheAspProLyLeuGlySerProGlnLeu 39
DB 61 CAGTGGGGGCGCAGGCTGGAGTTCGACCCGCGCGGAGACCCGACAGAGCTCGCC 120
QY 40 GluLeGluLeuAlaArgGlnAsnPheHLeuAspAsnArgPheThrHLeuSerAla 59
DB 121 GCCGTGAGCGCGCGCGCGCGGCTTCGGCGCGCGCGCGCAGAGCTCAAGCAGCTCC 180
QY 60 AspLeuLeuMetArgMet----- 65
DB 181 GACCTCTCATGCGCATGCGATGCGCGCGCGGCAATCAAACTGGGTAGCATGTTTAA 240
QY 66 -----GlnPheAlaArgGluAsnProThrArg 74
DB 241 GCCTTTATGAGCATGTAGAGATGACAGAACTCACTGTGCTAAACCAATCTCTTAAG 300
QY 75 GluValLeuProLyValGlyValLyAspGlyLeuAspValThrGlnGluValThr 94
DB 301 CTGACATTCACACTCAAGCTCAAGCTCAAGCAATGAAGCTTTCAAGCGCAAGCTGATTA 360
QY 95 LybThrLeuArgThrAlaValSerPheHLeuSerThrLeuGlnCysHLeuAspGlySer 114
DB 361 TCTCTCTAAAGGCGCAATGCTCGTATTCTACTTTTCACACATGATGACATCTGG 420
QY 115 ProGlyAspTyrGlyGlyProMetPheLeuMetProGlyLeuValLeuThrLeuSerIle 134
DB 421 CCTGGGATTAATGTTGGTCCCATGTTCTTATGCGAGCTTGATTAACATTAATATGTC 480
QY 135 ThrGlyAlaLeuAsnThrValLeuThrGlnGluHLeuArgLyGlnIleCysArgTyrLeu 154
DB 481 AGCGGAGCGCTGAACCTGCTTTGTCTACTGAAACATCAAGAGAGATACGGCGTATCTC 540
QY 155 TyrAsnHLeuGlnAsnLyAspGlyGlyTyrGlyLeuHLeuIleGlnGlyProSerThrMet 174
DB 541 TACATTCATCAAGATGAAGATGAGATGGGTTTGACATTGAGGGCGCACACACATG 600
QY 175 PheGlySerValLeuSerTyrIleThrLeuArgLeuGlnGlyGlyProAsnAspGly 194
DB 601 TTGGGCTCAGCGTTGACATATGTTCTTTGAGATTGCTTGCGGAGGGCGCAGTAGCGGC 660
QY 195 GlnGlyGluMetGlyLyAspAlaArgAspThrIleLeuGlyHLeuGlyAlaThrTyrIle 214
DB 661 GATGAGCTTAGAGAAAGACGAAATGATTTTACACATGGGGAGCACTTAATTT 720
QY 215 ThrSerTyrGlyLeuMetTyrLeuSerValLeuGlyValTyrGluTyrSerGlyAsnAsn 234
DB 721 ACATTCATGGGCAAGTTTGGCTTTGCGTCTTGCTGTATTTAGCTGCTGGAACAC 780
QY 235 ProLeuProGluIleTyrPheLeuProTyrMetLeuProPheHLeuProGlyArgMet 254
DB 781 CCAAGTCCACACAGAAATATGTTGTTGCTCATATTTCTGCGCATTCATCCAGCGCGCATG 840
QY 255 ThrCysHLeuCysAspMetValTyrLeuProMetSerTyrLeuTyrGlyLyAspPheVal 274
DB 841 TGGGTATTTGCCGAGATGTTATTTGCTTATGTTTACATTTATGGAAGAGGTTTGTG 900
QY 275 GlyProIleSerProThrValLeuSerLeuArgLyGlnLeuTyrThrValProTyrHLeu 294

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DB 901 GGGCCAGTTACACCAATATATGGAATTAGAAAGAACTCAAGATACCTACAT 960
QY 295 AspIleAspTyrAspGlnAlaArgAsnLeuCysAlaLyAspLeuTyrTyrProHLeu 314
DB 961 GAAGTTGATTTGGGACAAAGCTCGCAATTAATGTGTAAAGAAATCTTACTATCACAT 1020
QY 315 ProLeuValGlnAspIleLeuThrAlaSerLeuHLeuSerPheLeuGluProIleLeuMet 334
DB 1021 CCATTGCGAGAGATGATATGAGCCACTCTCCCAAAATTTGTTGAACAGCTATGTTG 1080
QY 335 HisTPProGlyLyAspGluArgGlyLyAspAlaIleLeuSerAlaLeuGlnHLeuHLeu 354
DB 1081 CGTTGGCTCGGAGAACAAATTAGGAGAAAGTTTGCACATGTCATGACAGATTTTCAT 1140
QY 355 TyrGluAspGluAsnThrArgTyrIleCysAlleGlyProValAsnValLeuAsnMet 374
DB 1141 TATGAAGATGAGAACACCCGATATATTTGCAATGTCGCAATGACAGATTAATATATG 1200
QY 375 LeuCysGlyTyrValGluAspProAsnSerGluAlaPheLyLeuHLeuProArgIle 394
DB 1201 CTGTGCTGCTGATTAAGATTCAAACTCAGAGGCAATTCAACTCCACATTCAGAGCTC 1260
QY 395 TyrAspTyrLeuThrIleAlaGluAspGlyMetLyMetGlnGlyTyrAsnGlySerGln 414
DB 1261 CACGATTCATTAATGATTCAGAAATGAGATGCAATGAATGCAAGGTTATATGAGAGCCAG 1320
QY 415 LeuTPAspThrAlaPheAlaValGlnAlaIleLeuAspAsnLeuIleGluGluPhe 434
DB 1321 CTGTGGACACAGCTTTCACTTCAGCTAATGAGTATGAGTCACTGAGCTCATTAAGAAATTT 1380
QY 435 GlyProThrIleArgLyAlaHLeuThrTyrIleLyAsnSerGlyValLeuGluAspCys 454
DB 1381 GGTCTTACTCTTAACTAGCACATGCGTACATTAAGAAACCCAGGTTATTCAGATGCTCC 1440
QY 455 ProGlyAspLeuAsnLybTyrArgHLeuSerIleSerLyGlyAlaTyrProPheSerThr 474
DB 1441 CCTGGAGATCTTAATGTCAGTGGTATGCGCCACATATCTTAAGGTGCATGGCCTTTCTACT 1500
QY 475 GlyAspHLeuGlyTyrProIleSerAspCysThrAlaGluGlyLeuLyAlaValLeu 494
DB 1501 GCGATTCATGATTTGGCTTATTCAGATTCATGCGCAGAGAGCATTAAGCGCATATATG 1560
QY 495 LeuSerLybIleAlaProGluIleValGlyGluProIleAspValLybArgLeuTyrAsp 514
DB 1561 CTATCGAAGATTTCTCCAGATATTTGTTGGCGAAGCGTGAAGTTAATGATGATGAT 1620
QY 515 SerValAsnValIleLeuSerLeuGlnAsnGluAspGlyGlyPheAlaThrTyrGluLeu 534
DB 1621 TCTGTCAAATGTTGATGTCATATGATGATGAATGATGATGATGATGATGATGATGATG 1680
QY 535 LybArgSerTyrAsnTyrPheGlnIleIleAsnProAlaGluThrPheGlyAspIleVal 554
DB 1681 ACAGAGTCTTAATGCGCTGGAGCTTATCAATCTCGTGAAGCCTTTGGGAGCATTTGG 1740
QY 555 IleAspTyrProTyrValGluCysThrSerAlaAlaIleGlnAlaLeuAlaSerPheArg 574
DB 1741 ATTGATTAATCCCTATGGAATGCACTTCAGACGCAATTCAGGCGCTGACAGCATTTAA 1800
QY 575 LybLeuTyrProGlyHLeuArgArgGluGluIleGlnHLeuCysValLeuAspLybThr 594
DB 1801 AAGCTTACCTCGGACACCGCAAGATGAATGAATGAATGAATGAATGAATGAATGAATGA 1860
QY 595 PheIleGluLybIleGlnAlaSerAspGlySerTyrTyrGlySerTyrGlyValCysPhe 614
DB 1861 TTTATTAAGGCTATTAAGAAACGATGTTTATGATGATGATGATGATGATGATGATGATG 1920
QY 615 ThrTyrGlyAlaTyrPheGlyValLyAspGlyLeuIleAlaAlaGlyArgSerPheSerAsn 634
DB 1921 ACCTATGGACATGATGTTGGTGAAGGATTAAGTGTGCTGCTGAGACATTCAAAAAC 1980
QY 635 CysSerSerIleArgLyAspAlaCysGluPheLeuLeuSerLybGlnLeuProSerGlyGly 654

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Db 1981 AGTCCTGCATCAGAAAGCATGTGACTTTTGTGTGCMAAAGACTCTCTTGAGGC 2040
QY TRPGIYGLUSERTYRLEUSERCYAGLNAENLYVALTYRSEARLENGLYANARG 674
Db 2041 TGGGAGAAAGCTATTGTGTATCCCAAGATCAGGTTTATACCAATCTCGAAGGAGCGA 2100
QY 675 SERHISVALIAENHTRGITYRPAIAEULEUALAULIENASPAAGLYGIALALYS 694
Db 2101 CCTATGGGGTGAACACTGGTGGGCGCATGCTAGCCCTATGATGACAGGGAGGCTGAG 2160
QY 695 ARGAPSERGLNPROLEUHIENARGALAAIAATYRLEUILEASERGLNLEUGLUSP 714
Db 2161 AGAGATCCAAATTCCTTGATGACAGGAGGATTTGATCACTTACATCGGAGAT 2220
QY 715 GLIAPRHEPROGLINGLULIEMETGLYVALPHEANLYSANCYMETIETHRTYR 734
Db 2221 GGTGAATTTCCCAACAGATCACTTGAGTCTTCAACAAATCTGATGATCGCTAC 2280
QY 735 AIAAATYRARGASNIENPHEPROILETRPALALEUGLYUTYRGLNSERGLNVALLEU 754
Db 2281 TCCGAGTATAGAAACATCTTCCCTATTGGGCGCTTGGGAGATACGTCGCGCTCTTG 2340

RESULT 9

US-10-425-114-24593
; Sequence 24593, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 24593
; LENGTH: 2653
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3632-042-C4_FLI
US-10-425-114-24593

Alignment Scores:

Pred. No.:	0	Length:	2653
Score:	3181.50	Matches:	568
Percent Similarity:	85.6%	Conservative:	79
Best Local Similarity:	75.1%	Mismatches:	97
Query Match:	76.7%	Indels:	12
	8	Gaps:	3

US-09-419-679-6 (1-757) x US-10-425-114-24593 (1-2653)

QY 1 MetTPLYSLLEUYSPHEALAGLU--GLYGLYANPRTOTRPLEUARGTHRLEUASN 19
Db 148 ATGTGGCCCTGCGGATGCGGAGGGGGGCGGAGACCCTGGCTCGGACGAAAGACCC 207
QY 20 HISVALIGLYARGGLNVALTRPGIUPHEAPPROLYSLEUGLYSERPROGLINAPLEU 39
Db 208 CACGTGCGCGCCAGAGTCTGGAGTTGAC-----GCCTTCGCGAGCCCGACCC 258
QY 40 GLIULEGLULYALARGLNAENPHEHISAPRANARGPETHRHISLYSHISERALA 59
Db 259 GCCGTGAGCGCGCGCGCGCGCTTCCGCGGACAGAGGGGCGACCTCAAGCAKCGCC 318
QY 60 APLEULEMETARGMETGLNPHENALARGGLUENPROTHRARGGLIVALLEUPROLYS 79
Db 319 GACCTTCATGATCGCATCCAGTTCCCAAGAAATTCCTTGACCTTGACCTTCCAGCG 378

QY 80 VALIGLYVALISAPRIEGLIAPSPVALTHRGINGLULIETHRYLSTHRLAARGARG 99
Db 379 ATCAAGCTCGGTAGCAGCAAGACGTAAACGAGAAACCCGTGTACTACTTATGAAAG 438
QY 100 AIAAIAERPHENHISERTHRLNGLNCYENHISAPRGLYHISSTPRPROGLYASRTYGLY 119
Db 439 GCAATCAGCGCTCTTTACTCTCCAGGCACATGATGACACTGCGGGGAAATATAGGT 498
QY 120 GLYPRHEC PHEUENMETPROGLYLEUVAILIETHRLEUSERILETHRGYVALALEUAN 139
Db 499 GGCCTTATGTTCTTATGCCAGGCTTATGATCACTATGATGATGATGATGATGATGAT 558
QY 140 THRVALLEUTHRGINGLUNHISARGLYEGULILECYAARGTYRLEUYRANHISGLASN 159
Db 559 ACTGTCTTGTCATCAGAACACCAAGAGAGATCCGCGGTATCTTTATATCATCAGAAAT 618
QY 160 LYSAPRGLYGLYTRPGIYLEUHIENGLUGLYPROSETHRMETPHEGLYSERVALLEU 179
Db 619 GAAGATGTGGCTGGGCTTGCACTTGAAGGTCCAAGACCAATGTTGGCTCAGACCTG 678
QY 180 SEPTYRILETHRLAARGLEUENGLYGLUGLYPROASNAPRGLINGLYLUMETGLU 199
Db 679 ACCTACGTTACTTTGAGATTGCTTGGAGAGGACCAATAGTGAATGAGACATGAG 738
QY 200 LYSALARGAPRTPRIELEUGLYHISGLYGLYALATHRYRILETHRSETRPGIYLYS 219
Db 739 AAAGCCGAAACTGATCTTAAGACCATGGCGAGCAATATATATCATCTCGGGGAG 798
QY 220 METTRPLEUSERVALLEUGLYVALTYRGLUTRPSERGLYASNANPPOLEUPROGLU 239
Db 799 TTTTGGCTCTCGGATCTGGGTGATTTGAAATGGCTGTGTAAACAACCCGATACCAAGAA 858
QY 240 ILETHRLEUENPOTRYMETLEUPROPHENISAPROGLYRPMETTRPYSHISCYAARG 259
Db 859 GTATGGCTACGCTCAATCTCTGCAATTCACCAAGAGAGATGGTGTATGTCGA 918
QY 260 METVALTYRLEUPROMETSEPTYRLEUTYRGLYLSARGPHEVALGLYPROILESERPRO 279
Db 919 ATGGTGATTTTGGCAAGTGCTACATCTATGAGGAAGGTTTGTGGTGAATACACCA 978
QY 280 THRVALLEUSERLEUARGLYEGULIENUTYRTHVALPROTYRHISAPRIEAPRTAPR 299
Db 979 CTCGTGTGGAATTAAGAAAGAACTTTTCAAGACCTTACAGCAAGATTGATGGGAC 1038
QY 300 GLINLARGASLEUCYSAIALYSGIUSPLEUUTYRTPROHISPROLEUVALIGLUSP 319
Db 1039 AAGGCCGCAATCATGTGCTAAGAGAAATCTGATCATCACTCACTTGTTCAGAT 1098
QY 320 ILEUTHRPLASERLEUHIISLYSPHELEUGLUPROILEUENHISTPRPROGLYLYS 339
Db 1099 GTCTTATGGCCACTCTCCATTAATTTGTGAACCACTTATGATGATGATGATGATGAT 1158
QY 340 ARGLEUARGGLYVALIALEIIESEVALALEUGLUNHISILEHISTYRGLIUSAPGLASN 359
Db 1159 AAATTGAGGAGAAAGCTGTGAGACAGACCATGCAACATGTTCACTGAGAGAGAGAAC 1218
QY 360 THRARGTYRILECYSLIEGLYPROVALASNLYSVALLEUENMETLEUCYSCYTRVAL 379
Db 1219 ACTCGGTACATTTGCATTTGCTGTGAACAAAGGTATTAATATAGCTTGTGCTGATTT 1278
QY 380 GLIUSAPROASNSEGLIUALAPHELYSLEUHIENLEUPROARGILETYRASPITYRLEUT 399
Db 1279 GAAGATCCAACTAGAGGCTTAAACTCCACATCCACAGAGCTATGACTACTTGTGG 1338
QY 400 ILEAIGLUSPGLIYMETLYMETGLINGLYTYRANGLYSEGLINLEUTHRASPRTALA 419
Db 1339 CTTCGTGAAGTGCATGAGATGACAGGTTATATATGATGACCACTTGGGATACAGCT 1398
QY 420 PHEALAVAGLIALAILEIIEASERASNLEUILEGLIUPHEGLYPROTHRILEARG 439
Db 1399 TTCATATGATCAAGCATTTGTGGCTAACCACTTACCAAGAGTTGTGCTCCACCTTAAA 1458
QY 440 LYSALAHISHTHRYRILELYSASNSEGLIVALLEUGLUSAPRCSYSPROGLYASPLEUAN 459

QY 80 ValGlyValIleuSerPheLeu-----ValThrGlnGluIleValThrIleuSer 97
 Db 232 GTGAAGAGTAAAGAGGCGAGAGAGATGATTAATGAAGAGATGATGATGATTA 291
 QY 98 ArgGlyAlaValSerPheIleSerThrLeuGlnCysHleAspGlyHleIleProGlyAsp 117
 Db 292 AGAAGAGAGTGAATGATTAATCTCAATCAATCAATCAATCAATCAATCAATCAAT 351
 QY 118 TyrGlyGlyProMetPheLeuMetProGlyLeuValIleThrLeuSerIleThrGlyAla 137
 Db 352 TATGGTGGCCCTTTGTTCTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 411
 QY 138 LeuAsnThrValLeuThrGlnGluHleAspGlyLeuIleCysArgGlyLeuThrAsnHis 157
 Db 412 TTGGATGGAACCTTAACTGGCAACATCAATGAGATTCGTCGATTAATCAATCAAT 471
 QY 158 GlnAsnIleAspGlyGlyTyrGlyLeuHleIleGlnGlyProSerThrMetPheGlySer 177
 Db 472 CAGAACAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGAT 531
 QY 178 ValLeuSerTyrIleThrLeuArgLeuLeuGlyGlyGlyProAsnAspGlyGlnGly 197
 Db 532 GTGCTCTACAGTACACCTGACACTAATGGGGAGAAATTAAGACGCTGAGATGAGCC 591
 QY 198 MetGlyValAlaArgAspTyrIleLeuGlnHleGlyAlaThrTyrIleThrSerTyr 217
 Db 592 ATGGATACAGCTGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 651
 QY 218 GlyIleMetTyrLeuSerValLeuGlyValTyrGlnTyrSerGlyAsnAspProLeuPro 237
 Db 652 GCGAAGTTCGGCTCTCCGTTCTTGGAGCTTATGAGTGGAGTGGAGAACATCTTTACCT 711
 QY 238 ProGlnIleTyrLeuSerProGlyMetLeuProPheHleProGlyArgMetTyrCysHis 257
 Db 712 CCAAGACTATGGCTCTCCATCAATAGTCTTCTTCAATCCGGCCGAAATGCTGCTCAT 771
 QY 258 CysArgMetValTyrLeuProMetSerTyrLeuTyrGlyValArgPheValGlyProIle 277
 Db 772 TGTAGATGGTTATATCTTCAATGTCATATCTAATGAGAGATTTGTTTGTCTGACT 831
 QY 278 SerProThrValLeuSerLeuArgLeuGlnLeuTyrThrValProTyrHisAspIleAsp 297
 Db 832 AATGGAACATATTTATGCTTCAACGAGAGCTCTACACTATCTTATCAACATATGAT 891
 QY 298 TyrAspGlnAlaArgAsnLeuCysAlaLeuGlyAspLeuTyrTyrProHisProLeuVal 317
 Db 892 TGGGACACCGCCCGTATCAATGTCAGAGAGAGATTTACTATCAATCCAAAGAT 951
 QY 318 GlnAspIleLeuTyrPheLeuSerLeuHlePheLeuGlnProIleLeuMetHisTyrPro 337
 Db 952 CAGACACCTCTTGGAGTGTCTGAAATTTTGGAGAGCTCTTCTTGAAGAATGGCCA 1011
 QY 338 GlyIleArgLeuArgGlyValAlaIleIleSerAlaLeuGlnHleIleIleTyrGlyAsp 357
 Db 1012 TTGAATAACTCAAGAACATGCTCTCAGACAGTATGCAACATTCATCACTAAGAGAC 1071
 QY 358 GlnAsnThrArgTyrIleGlyIleGlyProValAsnIleValLeuAsnMetLeuCysCys 377
 Db 1072 CAAACACGACCATATTTGATTCGCTCTGTCACAAAGCTTGAATATGCTTGTGT 1131
 QY 378 TyrValGlnAspProAsnSerGlnAlaPheLeuLeuHisIleLeuProAspGlyTyrAspTyr 397
 Db 1132 TGGGTGAGTCTCGAATTCGAGAGCATTAATCTCACTCTGCGGATTTAAAGATAT 1191
 QY 398 LeuTyrIleAlaGlnAspGlyMetLeuMetGlnGlyTyrAsnGlySerGlnLeuTyrAsp 417
 Db 1192 TTGGGTGGCTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1251
 QY 418 ThrAlaPheAlaValGlnAlaIleIleAsnSerLeuIleGlnGlyPheGlyProThr 437
 Db 1252 GTGACTTATGCGGTCAAGCAATCTGGCGAGAAATTTGTTGATGACTATGTTGATG 1311

QY 438 IleArgValAlaHisThrTyrIleLeuAsnSerGlnValLeuGlyAspProGlyAsp 457
 Db 1312 CTTAAGAAAGCCCATTAATCAATCAAGACATCAATTAAGAAAGACAAAGTGGAGAT 1371
 QY 458 LeuAsnIleTyrTyrArgHisIleSerLeuGlyAlaTyrProPheSerThrGlyAspHis 477
 Db 1372 CCGGGGTGTGGTACCGACACCCCGCAAGAGAGATGGGGTTCCTCCACGAGAACAT 1431
 QY 478 GlyTyrProIleSerAspCysThrAlaGlnGlyLeuValAlaIleLeuLeuSerIle 497
 Db 1432 CCATGGCTGCTCTGATTTGATCTGTAAGCTTGAAGGGCGCTTCTATTTGACAA 1491
 QY 498 IleAlaProGlnIleValGlyGluProIleAspValIleAspLeuTyrAspSerValAsn 517
 Db 1492 ATGCGGGTAAATTTAGTTGGAGAACCATGCTGTAAGAGCATTTAGTTGAGCTGTAAAC 1551
 QY 518 ValIleLeuSerLeuGlnAsnGlyAspGlyIlePheAlaThrTyrGlnLeuLeuArgSer 537
 Db 1552 TTTATCTTATCATTTACAGAACAAATGGGGATTTGGCTATATGAGCTAATGATCA 1611
 QY 538 TyrAsnTyrLeuGlnIleIleAsnProAlaGlnThrPheGlyAspIleValIleAspTyr 557
 Db 1612 TATCCCGAGCTGAGAGTTATCAACCATCAGAGCTTTTGGGATATCATATGATAT 1671
 QY 558 ProTyrValGlnCysThrSerAlaAlaIleGlnAlaLeuAlaSerPheArgIleuTyr 577
 Db 1672 CAATAGTAAGATGACGCTGACCTGCATCCAGGCTTCGTATTAATCAACGTTAAAT 1731
 QY 578 ProGlyHisArgArgGlnGluIleGlnHisCysIleAspValAlaThrThrPheIleGlu 597
 Db 1732 TCGAGCTACAAAGAGAGAGATGATGAGAGACATCAACAAAGCGTTGAGTTATGAA 1791
 QY 598 IysIleGlnAlaSerAspGlySerTyrGlyIleSerTyrGlyValCysPheThrTyrGly 617
 Db 1792 AAAACCAACTTCTGATGCTTCATGATGCTGCTGAGAGTGGTTCCTATGCA 1851
 QY 618 AlaThrPheGlyValIleGlyLeuIleAlaIleArgSerPheSerAsnCysSerSer 637
 Db 1852 ACATGGTTGATTAATTAAGAGATGTTGGCTCAGGCAAAACATATGAGAGCTTTGT 1911
 QY 638 IleArgValAlaCysGlnPheLeuSerIleGlnLeuProSerGlyGlyTyrGlyGlu 657
 Db 1912 ATTAAGAAAGCTTGGCTTCTGCTCCAAACACTTGTGTGGTGGATGGGAGAG 1971
 QY 658 SerTyrLeuSerCysGlnAsnIleValTyrSerAsnLeuGlnGlyAsnArgSerHisVal 677
 Db 1972 AGTACTCTTCTTCCAAACAAAGTATACCAATCTTCTGAGATTAATCGCATAT 2031
 QY 678 ValAsnThrGlyTyrAlaMetLeuAlaLeuIleAspAlaGlyGlnAlaValArgAspSer 697
 Db 2032 GTGACACATCATGGGACCTTGTGCTCATTTGAAGCGGAGCAAGCTGATGAGATCGG 2091
 QY 698 GlnProLeuHisArgAlaAlaAlaIleTyrLeuIleAsnSerGlnLeuGlyAspPhe 717
 Db 2092 ATGCCATTCATGCGCGGCGGCAAAATGCTGATCAATCCGACATGGAATGAGATTC 2151
 QY 718 ProGlnGlnIleMetGlyValPheAsnIleAsnCysMetIleThrTyrAlaAlaTyr 737
 Db 2152 CCACAAACAGAGATTAATGAGATCTTAATCGAAATTTGATGATGATGATGATGATGAT 2211
 QY 738 ArgAsnIlePheProIleTyrAlaLeuGlyGlyTyrGlnSerGlnValLeu 754
 Db 2212 AGAACAATATTCCTCCATTTGGCTTGGAGATACCGCAACTCATGTTG 2262

RESULT 12
 US-10-221-074-7
 ; Sequence 7, Application US/10221074
 ; Publication No. US20030208791A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bryan, Gregory T.
 ; APPLICANT: Hwang, Der-Chyan
 ; APPLICANT: Maxwell, Carl A.
 ; APPLICANT: McConigle, Brian

```
/ APPLICANT: Potter, Susan M.
/ TITLE OF INVENTION: ENZYMES INVOLVED IN TRITERPENE SYNTHESIS
/ FILE REFERENCE: B81438.PCT
/ CURRENT APPLICATION NUMBER: US/10/221,074
/ CURRENT FILING DATE: 2003-01-08
/ PRIOR APPLICATION NUMBER: 60/188,054
/ PRIOR FILING DATE: 2000-03-09
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: Microsoft Office 97
/ SEQ ID NO: 7
/ LENGTH: 2538
/ TYPE: DNA
/ ORGANISM: Trifolium aestivum
US-10-221-074-7

Alignment Scores:
  Score: 6,83e-286      Length: 2538
  Percent Similarity: 2551.00      Matches: 446
  Best Local Similarity: 77.64      Conservative: 139
  Query Match: 59.24      Mismatches: 163
  Db: 61.54      Indels: 6
  Gaps: 3

US-09-419-679-6 (1-757) x US-10-221-074-7 (1-2538)

Qy      1 MetTPrLLeuLysPheAlaGluGlyGlyAsnProTPrLLeuArgThrLeuAsnHis 20
Db      69 ATGTGAGAGCTCAAGGTGTCAGAGGAGTGGCGCCGTGGCTGGCTGGTGAACAATTC 128

Qy      21 ValGlyArgGlnValTPrGluPheAsnProLysLeuGlySerProGlnAspLeuGlu 40
Db      129 CTCGGCAGGAGGAGTGTGGGAGTTTCAGCCCGCATCGGACACCGGAGAGCGCCGAG 188

Qy      41 ILeGluLysAlaArgGlnAsnPheHisAspAsnArgPheThrHisLysHisSerAlaAsp 60
Db      189 GTGAAGAGGAGTGGCGGAGAGTTTCACGACCGCTTTGAGAAAAAGAGTCGCGAGAT 248

Qy      61 LeuLeuMetArgMetGlnPheAlaArgGluAsnProThrArgGluValLeuProLysVal 80
Db      249 CTTTCATGCGCATCATGATGATCAAAAGAAAGCATCTTCAGGTGGACCTTCACGCCATC 308

Qy      81 GlyValLysAspIleGluAspValThrGlnGluIleValThrLysThrLeuArgHisAla 100
Db      309 AAGCTTGACAGACAGTGCACAGTGCACAGAGAGCATTTACTAACAATCTTAGAGCGAGATC 368

Qy      101 ValSerPheHisSerThrLeuGlnCysHisAspGlyHisSTPrProGlyAspTyrGly 120
Db      369 CTTAGCCCAATTCCTGCTCTACAGACACAGATGGGCAATGGGCTGGGACCTTCAGTGA 428

Qy      121 PrometPheLeuMetProGlyLeuValIleThrLeuSerIleThrGlyAlaLeuAsnThr 140
Db      429 ATTGTGTCATTATGCCCATCTTGAATTTGCTCTACATGTTACTCGATCACTCAATACT 488

Qy      141 ValLeuThrGlnGluHisArgLysGluIleCysArgTyrLeuTyrAsnHisGlnAsnLys 160
Db      489 GTCCCATCAACAGAACATCGATGATGATTTGTCCCTATATTACACATCAAGAAATGA 548

Qy      161 AspGlyLysTPrGlyLeuHisIleIleGluGlyProSerThrMetPheGlySerValLeuSer 180
Db      549 GATGTGTGGTGGGACGACCAAGTGTGGGTCCGACACCAATGTTTGATCATGCTTAAC 608

Qy      181 TyrIleThrLeuArgLeuLeuGluGlyGluProAsnAspGlyGlnGlyIleMetGlnLys 200
Db      609 TATGTATACCTTAAGGCTTCTTGGCGAGGTGAGAAATGATGCC-----TTAACCAAG 659

Qy      201 AlaArgAsnProTPrIleLeuGlyHisGlyGlyAlaThrTyrIleThrSerTPrGlyLysMet 220
Db      660 GACGTGTGCTGATTTCTATGCGTGAAGTGCATTCGCAATACCAATGGGAAAGATA 719

Qy      221 TrpLeuSerValLeuGlyValTyrGluTPrSerGlyAsnAsnProLeuProGluIle 240
Db      720 TGGCTCTCGGTGGTGGTTTATATGATGATGCTGAGAAATTAATTGATCATTCCTGAGTTA 779
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Qy      241 TrpLeuLeuProTyrMetLeuProPheHisProGlyArgMetTPrCysHisCysArgMet 260
Db      780 TGGCTTGCCCGATTTTCTTCGATTCATCCAGAGCATTCGTGCTTTTGGCCGGTGG 839

Qy      261 ValTyrLeuProMetSerTyrLeuTyrGlyLysArgPheValGlyProIleSerProThr 280
Db      840 GTTATATGCCAAAGTCTTATCTTTACGGCAAAAAGTTTGTGGCCAAATTAACACACA 899

Qy      281 ValLeuSerLeuArgLysGluLeuTyrThrValProTyrHisAspIleAspTPrAspGln 300
Db      900 ATAGTGCATATAGAGAGAGCTCTTATGATGATCATACAGCGAGATTTGATGACAA 959

Qy      301 AlaArgAsnLeuCysAlaLysGluAspLeuTyrTyrProHisProLeuValGlnAspIle 320
Db      960 GCACGTATATCTTGCTTGAAGAGACCTTCGATACAGGTGCTTGCTGCAAAATGTT 1019

Qy      321 LeuTPrAlaSerLeuHisLysPheLeuGluProIleLeuMetHisSTPrProGlyLysArg 340
Db      1020 ATTGGACTTGCCCTTAATAATTTGTGAACCAAGTGTGAATGTTGGCCCAATCAATAG 1079

Qy      341 LeuArgGluLysAlaIleIleSerAlaLeuGlnHisIleHisTyrGluAspGluAsnThr 360
Db      1080 TTGAGAGATACAGCGCTGAAGAACCTCATGAAACATATACATTAAGAGCAAGACACT 1139

Qy      361 ArgTyrIleCysIleGlyProValAsnLysValLeuAsnMetLeuCysCysTPrValGlu 380
Db      1140 AAATACATTTGGCGATATCCGATTTACAGAGCACTAATATGATTTTGTGGAGGAGC 1199

Qy      381 AspProAsnSerGlnAlaPheLysLeuHisLeuAspProArgIleTyrAspTyrLeuTPrIle 400
Db      1200 GATCCAAATTCAGATGACATGAGATGATTCATCTTCACAGATCTATATGACTTTATGCTT 1259

Qy      401 AlGluAspGlyMetLysMetGlnGlyTyrAsnGlySerGlnLeuTPrAspThrAlaPhe 420
Db      1260 GCAGAAAGATGGCATGAAGAACAGAGTTATGATGAGTTGTCAAAAGCTGGAGCTTCTTT 1319

Qy      421 AlaValGlnAlaIleIleAlaSerAsnLeuIleGluGluPheGlyProThrIleArgLys 440
Db      1320 ATTGTCACATATTCCTGTCAGACAGCTTGTTAATGATTTGGTCCAAACCTTCGAAA 1379

Qy      441 AlaHisThrTyrIleLysAsnSerGlnValLeuGluAspCysPProGlyAspLeuAsnLys 460
Db      1380 GCCCATGATTCATTAATAAGTTCACAGGTTCTTGAGAAACATCTTAACAGT---GAAACT 1436

Qy      461 TrpTyrArgHisIleSerLysGlyAlaTPrProPheSerThrGlyAspHisGlyTPrPro 480
Db      1437 TATTACCGCATATAGTCAAAAGGTTCATGAGACCTTTCACACAGCGGATTAATGGGTGCT 1496

Qy      481 IleSerAspCysThrAlaGluGlyLeuLysAlaValLeuLeuLeuSerLysIleAlaPro 500
Db      1497 GTATCAGATTGTACTGCAGAAAGCACTTAAGGCATTTGTTGTTGTGGAAGATCTCTCT 1556

Qy      501 GlnIleValGlyGluProIleAspValLysArgLeuTyrAspSerValAsnValIleLeu 520
Db      1557 AATCTGTGGGGGATCCCGTAAAGAGAAAGGTGATGATGACATGCGATTCGTTACTT 1616

Qy      521 SerLeuGlnAsnGluAspGlyGlyPheAlaThrTyrGluLeuLysValGlySerTyrAsnTPr 540
Db      1617 TCTTTATGATATGAATGACATTTTCTACATATGAGTGAAGTAAGAACTCAATCTCTA 1676

Qy      541 LeuGluTyrIleLeuAsnProAlaGluThrPheGlyAspIleValIleAspTyrProTyrVal 560
Db      1677 TTAGAGGTCTCAACCTTCTGAAAGTTTCTGAAACATTTATGTCGACTATCCATCTGTC 1736

Qy      561 GlnCysThrSerAlaAlaIleGlnAlaLeuAlaSerPheArgLysLeuTyrProGlyHis 580
Db      1737 GAATGTCATCATCATCTGCTTCAGAGCCCTAATATGTTCAAAAGAGCTTTACCCGGGTAC 1796

Qy      581 ArgArgGluGluIleGlnHisCysIleAspLysAlaThrThrPheIleGluLysIleGln 600
Db      1797 CGCAAAAGAAAGATGAGAAATGATTAATAAAAGCTTCCAAGTTTCAATGAGAGCAACAA 1856

Qy      601 AlaSerAspGlySerTPrTyrGlySerTPrGlyValCysPheThrTyrGlyAlaTPrPhe 620
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Db      1857 CGAAGAGTGGCTTGGCTTTGGCACTTGGGTATATGTTTCACTTATGAGGAGCTTCTT 1916
Qy      621 GIVAlVbGVLyLeuIlleAlaIaGlyArgSerPheSerAsnCySerSerIleArgLys 640
Db      1917 GGTGTAAAGAGATTGATGCTTCTTGGAGAACTTGAAGAAATAGTCTTCCATTAGGAAA 1976
Qy      641 AlAcYbGVLuPheLeuLeuSerLysGlnLeuProSerGlyGlyTTPGlyGlnuSeryLeu 660
Db      1977 GCATCAATTTTCTGTGTCAAGAGCACTAGACAGGGATGAGTGGAGAGCTTATCTT 2036
Qy      661 SerCybGlnAsnLysValTyLysSeruLeuGlnGlyAsnArgSerHisValValenThr 680
Db      2037 TCTAGTGAACCTGAGGCTTAT-----GTGAGGCGCACTAGTCTCATGCACTGAACCT 2090
Qy      661 GIVTPAlaMetLeuAlaLeuIleAspAlaGlyGlnAlaLysArgAspSerGlnProLeu 700
Db      2091 GCTTGGGCAATGTGGCTTTATTTATGCTGGGCAAGTTGAACGAGATCTTCACTCACTA 2150
Qy      701 HisArgAlaAlaAlaTyLysLeuIleAsnSerGlnLeuGlnAspGlyAspPheProGlnGln 720
Db      2151 TATCATGCTGCAAAAGAGTTGATCATATGCAACTAGAGACAGAGAGTTTCCCGACGAA 2210
Qy      721 GlnIleMetGlyValPheAsnLysAsnCySerMetIleThrTyAlaAlaTyArgAsnIle 740
Db      2211 GAACACGTTGAGTGTCTCAACTGCTCCATATACTTTATTTACGGCAACTATGCACTTA 2270
Qy      741 PheProIleTPAlaLeuGlnGlyGlyTyArgInsSerGlnValLeu 754
Db      2271 TACCCATTGGGCTCTTGGGAGATTGCTGTGCACTGCTT 2312

RESULT 13
US-10-425-114-24645
/ Sequence 24645, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jindong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E
/ APPLICANT: Tabaka, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(5313)B
/ CURRENT APPLICATION NUMBER: US/10/425, 114
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 24645
/ LENGTH: 2593
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURe:
/ OTHER INFORMATION: Clone ID: LIB3632-052-FL_FLI
US-10-425-114-24645

Alignment Scores:
Pred. No.: 5,3e-285 Length: 2593
Score: 2543.50 Matches: 444
Percent Similarity: 77.4% Conservative: 138
Best Local Similarity: 59.0% Mismatches: 167
Query Match: 61.3% Indels: 3
DB: 8 Gaps: 2

US-09-419-679-6 (1-757) x US-10-425-114-24645 (1-2593)
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Db      69 ATGTGAGAGGCTGACGGTGGCGAGGGCGGCCCGGTGGCTGCGCTGACGAGACGGCTTC 128
Qy      21 ValGlyArgGlnValTTPGlnPheAspProLysLeuGlnSerProGlnAspPheLeuGln 40
Db      129 GTGGGCGCGCGGTGTGGAGTTGACCTTGACCTCGGTACGCCGAGAGCGCGACGAG 188

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Qy      41 IleGlnLysAlaArgGlnAsnPheHisAspAsnArgPheThrHisLysHisSerAlaAsp 60
Db      189 GTAGAGAGGGTAAACCCAGAGATTTCCGACCAACGGCTTCCAGAGAGAGAGATCGGCCAC 248
Qy      61 LeuLeuMetArgMetGlnPheAlaArgGlnAsnProThr---ArgGlnValLeuProLys 79
Db      249 CTCCTCATGCCCATGCACTGCGGCAAGAGCAAGATCTCAACGTCGTGATCTGGACAGC 308
Qy      80 ValGlyValLysAspIleGlnAspValThrGlnGlnIleValThrLysThrLeuArgArg 99
Db      309 ATCAAGCTTGGGAGAGATGAGACAGCTCACTAGAAATTTGACTGAGCTCTTGAGGTCG 368
Qy      100 AlaValSerPheHisSerThrLeuGlnCysHisAspGlyHisTTPProGlyAspTyGly 119
Db      369 GCTTGAGCAAGTCTCTCACTGCAACCCAGCGAGTGGCACTGGCTGTGATTTTCACG 428
Qy      120 GlyProMetPheLeuMetProGlyLeuValIleThrLysSerIleThrGlyAlaLeuAsn 139
Db      429 GGGATTATGTTCAATCATGCTGTTGATTTGCTTGTATTTGCTGTGATGTCAGTCACTGAT 488
Qy      140 ThrValLeuThrGlnGlnHisArgLysGlnIleCysArgTyLLeuTyArgHisGlnAsn 159
Db      489 GTTGTCATATCACAGAACATCGCATGATGATTGCCCTACATCTACACACACAGAAC 548
Qy      160 LysAspGlyGlyTyTPGlyLeuHisIleIleGlnGlyProSerThrMetPheGlySerValLeu 179
Db      549 GAAGATGTGGATGGGGGCACTTATCTTGAGTTCGACACACCATTTTGGCAACATCTTCA 608
Qy      180 SerTyIleThrLeuArgLeuLeuGlnGlyGlyTyProAsnAspGlyGlnGlyLysMetGln 199
Db      609 AACTACATACCTTGAAGGCTTCCGTGAGAGCCATACGCAACAGATGTTGGGT 668
Qy      200 LysAlaArgAspTTPIleLeuGlnLysIleGlyAlaThrTyIleThrSerTTPGlyLys 219
Db      669 AAGGGCGTGTGATGTTCTATCCATGATGTCGAACTTGATTTCTCAGTGGGAGAAA 728
Qy      220 MetTTPLeuSerValLeuGlnValTyArgLutPSPSerGlyAsnAsnProLeuProProGln 239
Db      729 ATATGGCTTTCGGTCTTGATGTTGATTTGATGGTCAAGAAATTAATCAATTTTCCCTGAA 788
Qy      240 IleTTPLeuLeuProTyLysMetLeuProPheHisProGlyArgMetTTPCysHisCysArg 259
Db      789 CTATGCTCATTCCTCCAGTGTCTTCCATTTTCCAGGGAAATTTGCGTGGCTTGGCCGT 848
Qy      260 MetValTyLysProMetSerTyLeuTyArgLysArgPheValGlyProIleSerPro 279
Db      849 ATGATATATCAACAATGCGCTTATGTCAGAAATTTGTTGACCAATTTACACCA 908
Qy      280 ThrValLeuSerLeuArgLysGlnLeuTyThrValProTyHisAspIleAspTTPAsp 299
Db      909 ACTATATGCACTAAGAGAGAAATCTATGACACTCTTATGAAAGATTTTACCTGAGCT 968
Qy      300 GlnAlaArgAsnLeuCysValAlaLysGlnAspLeuTyTyThrProHisProLeuValGlnAsp 319
Db      969 GATGCTGTAGTAAAGCCCAAGAGAGACCTCATGTCACAGCCACACTGTTCGCAAT 1028
Qy      320 IleLeuTTPAlaSerLeuHisLysPheLeuGlnProIleLeuMetHisTTPProGlyLys 339
Db      1029 GTTATTTGACCTTCACTTTATAGTGTGTGGAACAGATTTGACAGTGTGGCTATCAAC 1088
Qy      340 ArgLeuArgGlnLysAlaIleIleSerAlaLeuGlnHisIleHisTyGlnAspGlnAsn 359
Db      1089 AAGCTGAGAGAGAGACTCTGGGAAACATCATGACATGACATATTCATTTAGATGAGAAC 1148
Qy      360 ThrArgTyIleCysIleGlyProValAsnLysValLeuAsnMetLeuCysTyTTPVal 379
Db      1149 ACACAATACCTTATGCAATATGCTGTGAATTAAGCTTTAAACATGTGCTCTGCTGGGTA 1208
Qy      380 GlnAspProAsnSerGlnAlaPheLysLeuHisIleLeuProArgIleTyArgAspTyLys 399
Db      1209 GAAGATCCAAATTCATATGATTCAGAGCGTCACTTGCAGAGATACAGAGCTTCTGTGG 1268

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400 IleaAlaGluAerPGlyMeIyWeIcInGlyTyTyraNGlySerGlnLeuTrpAerThraLa 419
1269 ATTTCAGAAAGATGCGATGAGCACAAGATATGATGCTGCGACAGAGCTGGAGACATCA 1328
420 PheAlaValGlnAlaIleIleAlaSerAenIleuIleGluInPheGlyProThrIleArg 439
1339 TTCATATATTCAGCAATTTTGGCTACAGATCTGTAAATGACTATAGGTTCACACTCTTCAG 1388
440 LysAlaHisThrTyTyleYAsnSerGlnValIleGluAerPGlyAspLeuAen 459
1389 AGAGCTTATGACTTATGAAATTCACAGGTCATAGAGAACATCTCGTGCACCAAGT 1448
460 LysTrpTyTargHisIleSerIyGlyAlaTrpProPheSerThrGlyAspHisGlyTrp 479
1449 TATTTGGCATCGCCATAGATCGAAGGGTTTCATGACACTTTCATCTGCAGACATGATGG 1508
480 ProIleSerAerPGlyThrAlaGluIleuYsAlaValIleuLeuLeuSerIyAla 499
1509 GCTGATCTGCATACAGAGAGAGACACTTAAGCTGATCTGTGCTGCACAAAGATCTCA 1568
500 ProGlu-----IleValGlyGluProIleAerValYsArgLeuTyTAspSerValAen 517
1569 AACAAACAAACACTTGTGGGATCCATAGAAAGAAAGGTTGCATGACGCTATTCAT 1628
518 ValIleuSerLeuGlnAenGluAerPGlyGlyPheAlaThrTyTyluLeuYsArgSer 537
1629 TGCCCTTATCTTTTGGCAACAAAGATGGACCTTTTTCATATAGTGCACAAAGAACT 1688
538 TyTAsnTrpLeuGluIleIleAenProAlaGluThrPheGlyAspIleValIleAerTyT 557
1689 TATTTGGGTAAAGAAATTCAGATCTTGTGAGACTTTCACAAACATTTGTGTCATTAAT 1748
558 ProTyTValGlyCyTThrSerAlaIleGlnAlaLeuAlaSerPheArgLeuYsLeuTyT 577
1749 CCTTACCAAGATGACATTCATCACTGCTCCAGCTCGATATTTTTCAAACACTTAAT 1808
578 ProGlyNlsArgArgGluGluIleGlnHisCyTleAerPheAlaThrThrPheIleGlu 597
1809 CCTGTATCCGACAGAAAGATAGACATTAAGTGAAGTGCAGCAACGTTTATTTAG 1868
598 LysIleGlnAlaSerAerPGlySerTrpTyTyluSerTrpGlyValCyTPherThrTyTylu 617
1869 ACCAAACAAACAAAGACGGTTCAAGGTGAATGGGATATGGGATATGTTTCACTACCGG 1928
618 AlaTrpPheGlyValYsGlyLeuIleAlaIleArgSerPheSerAenCySerser 637
1929 GCCTCTTTTGCATTAAGGTTTACGCTCTGGAAGACATACAAAGACGCTTGC 1988
638 IleArgYsAlaCySgluPheLeuLeuSerIyGlnLeuProSerGlyTyTTrpGlyGlu 657
1989 ATACGGAAGATGCGCACTTCATATTTGTCGAAGCAGCTCAGTACGTGGTGAATGGGAGAA 2048
658 SerTyTLeuSerCySgluAenYsValTyTserAenLeuGluYsAenArgSerHisVal 677
2049 AGCCATATCCGCTATTAAGAACTCAAGGTGATGTAAATTCCAAGAGGACCGTCTCACCT 2108
678 ValAenThrGlyTyTTrpAlaMetLeuAlaLeuIleAerAlaGlyGlnAlaYsArgAerSer 697
2109 GTGAATACCGCTGGGCAATGCTCGCTTAATTTATGCTGACACATTTGAAGACGAAATCA 2168
698 GlnProLeuNlsArgAlaAlaAlaTyTleuIleAenSerGlnLeuGluAerPGlyYsAerPhe 717
2169 ACGCATTAACATCGTGGTGCAGAAAGAAATTCATCAACATGCACTGGAACAGAGAGTTT 2228
718 ProGlnGlnGluIleMetGlyValPheAenYsAenCySmetIleThrTyTAlaAlaTyT 737
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US-10-425-115-65768
; Sequence 65768, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425, 115
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 65768
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_159985C.1
US-10-425-115-65768
Alignment Scores:
Pred. No.: 5,41e-285 Length: 2627
Score: 2543.50 Matches: 444
Percent Similarity: 77.4% Conservative: 138
Best Local Similarity: 59.0% Mismatches: 167
Query Match: 61.3% Indels: 3
DB: Gaps: 2
US-09-419-679-6 (1-757) x US-10-425-115-65768 (1-2627)
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QY 140 ThrValLeuThrGluGluNlsArgYsGluIleCySArgTyTleuTyTAsnHisGlnAen 159
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QY 200 LysAlaArgAerTrpIleLeuGluNlsGlyValAthrTyTleThrSerTrpGlyYs 219

40 ATGTGAGGCTGAGATGACAGATGAGAGAAATGATCCATACATATTCAGCAAAACAT 99
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Db 100 TTCGTTGGAGGACACATGGAGATTGATCTTGAAAGCAGGAGCTCCAGAGAAAGGAGCC 159
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Db 760 GAGTTTGGATCTCTCCATCTTCTCTCTATGATCCAGCTAAGATGTGGTATCTGT 819
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Db 820 CGATTGGATACATGCTATGCTTATATATGGAAGAGTGTGGTCAATGCA 879
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Db 880 CCACTCATCTTAACAATTAAGAGAGAGTGTATCTCAACCTTAAGAAAAGTTAATGTG 939
Qy 299 AspGlnAlaAspAspLeuCysAlaLysGluAspLeuTyrTyrProHisProLeuValGln 318
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Qy 319 AspIleLeuTyrAlaSerLeuHisLysPheLeuGluProIleLeuMetHisTyrPro-- 337
Db 1000 GACCTAAATATGGATATGTTTATACATATTCACCTGAACCGCTAATCTGTTGGCGTTTC 1059
Qy 338 GlyLysValGlyLeuArgGlyLysAlaIleIleSerAlaLeuGlnHisIleTyrGluAsp 357
Db 1060 AACAAAGTATTAAGAAAGAGCGCTTCAAGTAACTAAGAACTATTAATTAAGAAAT 1119
Qy 358 GlnAspThrArgTyrIleCysIleGlyProValAspValLeuAspMetLeuCysCys 377
Db 1120 GAGACTAGTCAATACATACCAATGGTGTGTGGAAAGGTTTTATGATAGTCTGCTTGT 1179

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Db 1180 TGGGTGGAAGATCCAAACGAGATGCTTCAAGAAAGATCTTCAAGAGGTCCAGATTAC 1239
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Db 1240 TTATGGGTTCCTGAAGATGGAATGACATGACAGATTTT--GGTACCAAGAAATGGGAT 1296
Qy 418 ThrAlaPheAlaValGlnAlaIleIleAlaSerAsnLeuIleGluGluPheGlyProThr 437
Db 1297 GTCGCTTGTGCTGTTCAAGCTTGTCTGCACTAACATTAATTAAGAAATTTGTCCTACG 1356
Qy 438 IleArgLysAlaHisThrTyrIleLysAspSerGlnValLeuGluAspCysProGlyAsp 457
Db 1357 TTTCAGAAAGCACTGATTTTCATCAAGAGTCTCAGGTGAAGATATTCCTTTGGAGAT 1416
Qy 458 LeuAsnLysTyrTyrArgHisIleSerLysGlyAlaTyrProPheSerThrGlyAspHis 477
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Db 1537 TTGGCACCAAGATTTGGAGAGAAAGATGGAACCTGAAGATTAATACGATTCAGTCAAT 1596
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Db 1597 GTCCTGTTGTCGCTTCAAGATTAAGGTTGTTTACACATGGAGCTGACAGAGCT 1656
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Qy 578 ProGlyHisArgArgGluGlnIleGlnHisCysIleAspLysValAlaThrPheIleGlu 597
Db 1777 CCAAGACATAGAGAGAAAGATAGAAATTTCTATCAATCAAGATTCGATTCCTTGA 1836
Qy 598 LysIleGlnAlaSerAspGlySerTyrGlyIleSerTyrGlyValCysPheThrTyrGly 617
Db 1837 GATACACAAACAGCTGATGTTTCATGTATGGAATGGGAGATTTCTTCATATGTC 1896
Qy 618 AlaThrPheGlyValLysGlyLeuIleAlaAlaGlyLysArgPheSerAsnCysSerSer 637
Db 1897 TCTTGGTTTGCACTTGAAGGCTTAGCGCTGCTGTAAGACTTAACACCAATTTGCTGCC 1956
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Qy 658 SerTyrLeuSerCysGlnAsnLysValTyrSerAsnLeuGluGlyAspAspSerHisVal 677
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Qy 678 ValAsnThrGlyTyrAlaMetLeuAlaLeuIleAspAlaGlyGlnAlaLysArgAspSer 697
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Tue May 23 09:40:23 2006

us-09-419-679-6.p2n.rnpbm

Page 21

Qy		738	ArgAsnIlePheProIleTrrPalaleuglyGluTrgInserGlnVal	753
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Job time : 2041 sec

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GenCore version 5.1.8
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OM protein - nucleic search. using frame p2n model

Run on: May 22, 2006, 21:49:42 ; Search time 353 Seconds
(without alignments)
6018.822 Million cell updates/sec

Title: US-09-419-679-6

Perfect score: 4148
Sequence: 1 MWKLFARAGGNPMTLNNH.....RNIPFALGYSQVLSR 757

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Command line parameters:
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss09p -USER=6630617@CGN.1.1.307@runat.19052006.165940.28573 -NCPU=6
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Database : Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	4148	100.0	2560	US-09-419-679-5	Sequence 5, Appl1
2	3125	75.3	2558	US-09-419-679-1	Sequence 1, Appl1
3	2433	58.7	1882	US-09-419-679-3	Sequence 3, Appl1
4	1653.5	39.9	4346	US-09-919-039-112	Sequence 112, App
5	1597	38.5	4239	US-09-815-048-1	Sequence 1, Appl1
6	1442	34.8	1300	US-09-419-679-7	Sequence 7, Appl1
7	1276	30.8	2196	US-09-614-221A-308	Sequence 308, App
8	403.5	9.7	747	US-09-248-796A-3811	Sequence 3811, Ap

C	9	361	8.7	536165	3	US-09-214-808-1	Sequence 1, Appl1
C	10	340.5	8.2	539	3	US-08-998-416-229	Sequence 229, App
C	11	329	7.9	1512	5	US-09-974-300-1079	Sequence 1079, Ap
C	12	302	7.3	652	3	US-09-533-559-4882	Sequence 4882, Ap
C	13	198	4.8	2072	3	US-09-725-735A-11	Sequence 11, Appl
C	14	168.5	4.1	3600	3	US-10-104-047-1011	Sequence 1011, Ap
C	15	165	4.0	173	3	US-09-313-294A-804	Sequence 804, App
C	16	158	3.8	42450	3	US-09-815-048-3	Sequence 3, Appl1
C	17	151	3.6	255	3	US-09-248-796A-3810	Sequence 3810, Ap
C	18	145.5	3.5	5046	3	US-09-725-735A-13	Sequence 13, Appl
C	19	121	2.9	33140	3	US-09-556-002-23	Sequence 23, Appl
C	20	118.5	2.9	1401	3	US-09-583-110-684	Sequence 1847, App
C	21	118.5	2.9	1419	3	US-09-107-433-1867	Sequence 1867, Ap
C	22	116	2.8	1306	3	US-09-387-574-3	Sequence 3, Appl1
C	23	116	2.8	1306	3	US-09-668-096-3	Sequence 3, Appl1
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C	25	113.5	2.7	7939	3	US-08-961-527-9	Sequence 9, Appl1
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C	40	109.5	2.6	7860	3	US-09-526-193A-2	Sequence 2, Appl1
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C	42	109.5	2.6	11282	2	US-09-059-853-1	Sequence 1, Appl1
C	43	109	2.6	11282	3	US-09-754-250-3	Sequence 3, Appl1
C	44	109	2.6	111282	3	US-10-094-989-3	Sequence 3, Appl1
C	45	108	2.6	14335	3	US-09-596-002-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-09-419-679-5
Sequence 5, Application US/09419679

Patent No. 6630617
GENERAL INFORMATION:

APPLICANT: Falco, S. Carl
APPLICANT: Pamodu, Omolayo O.
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Rafalski, Antoni
APPLICANT: McGonigle, Brian
APPLICANT: Lohman, Karin
TITLE OF INVENTION: Enzymes Involved In Squalene Metabolism
FILE REFERENCE: B0113 US NA
CURRENT APPLICATION NUMBER: US/09/419,679
CURRENT FILING DATE: 1999-10-15
EARLIER APPLICATION NUMBER: 60/105,405
EARLIER FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Microsoft Office 97
SEQ ID NO 5
LENGTH: 2560
TYPE: DNA
ORGANISM: Glycine max
US-09-419-679-5

Alignment Scores:

Pred. No.: 0
Percent Similarity: 4148.00
Best Local Similarity: 100.0%
Query Match: 100.0%
Length: 2560
Matches: 757
Conservative: 0
Mismatch: 0
Indels: 0

DB: 3 Gaps: 0
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DB 85 GTGGAAAGCAAGGTGGAGATTGCATCTTAAGCTTGAATGCCCGCAAGATCTCTCGAG 144
QY 41 IleGluLysAlaArgGlnAsnPheHisAspAsnArgPheThrHisLeuHisIleSerAlaAsp 60
DB 145 ATTTGAAAGAGCTCGCCAGAAATTTTCAAGATAACGGCTTTACCCACAAACACAGCGCTGAT 204
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DB 265 GAGATTTAAGATATTTGAGAGATGTGACCCCAAGATTGTGACAAACAAATTAAGAAAGGCC 324
QY 101 ValSerPheHisSerThrLeuGlnCysHisAspGlyHisIleTrpProGlyAspTyrGlyLys 120
DB 335 GTTAAGTTTCCATTCAACTCTCCAGTCCCATGACGACACACTGCGCGAGATTTATGGAGGT 384
QY 121 ProMetPheLeuMetProGlyLeuValIleThrLeuSerIleThrGlyValAlaLeuAsnThr 140
DB 385 CCCAATGTTCTGATCCCTGGCTTGGTAAATTACTGTCTATCATCATGGGGCGTTGAATTACA 444
QY 141 ValLeuThrGlnGluHisArgLysGluIleCysAspGlyTrpLeuThrAsnHisGlnAsnLys 160
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QY 341 LeuArgGluLysAlaIleIleSerAlaLeuGlnHisIleHisTyrGluAspGluAsnThr 360

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 US-09-419-679-1
 / Sequence 1, Application US/09419679
 / Patent No. 6630617
 / GENERAL INFORMATION:
 / APPLICANT: Falco, S. Carl
 / APPLICANT: Pamodu, Omolayo O.
 / APPLICANT: Kinney, Anthony J.
 / APPLICANT: Rafalski, Antoni
 / APPLICANT: McGonigle, Brian
 / APPLICANT: Lohman, Karin
 / TITLE OF INVENTION: Enzymes Involved in Squalene Metabolism
 / FILE REFERENCE: B0113 US NA
 / CURRENT APPLICATION NUMBER: US/09/419,679
 / EARLIER FILING DATE: 1999-10-15
 / EARLIER APPLICATION NUMBER: 60/105,405
 / EARLIER FILING DATE: 1998-10-23
 / NUMBER OF SEQ ID NOS: 16
 / SOFTWARE: Microsoft Office 97
 / SEQ ID NO 1
 / LENGTH: 2558
 / TYPE: DNA
 / ORGANISM: Zea mays
 US-09-419-679-1
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 Percent Similarity: 88.9% Conservative: 78
 Best Local Similarity: 77.7% Mismatches: 0
 Query Match: 75.3% Indels: 0
 Gaps: 0
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 Qy 74 ArgGluValLeuProLysValGlyValLysAspIleGluAspValThrGlnGluIleVal 93
 Db 63 GACCTTCACCTTCACAGCATCAAGCTCGGTGAGCATGAGATGATGACCGAGAAAGCTGTG 122
 Qy 94 ThrLysThrLeuArgAlaValAspPheHisSerThrLeuGlnCyHisAspGlyHis 113
 Db 123 TTACATCAACATTGAAGAGGCAATCAAGCGCTTCTCATCTCTCCAGGCAATGATGAGCAC 182
 Qy 114 TTPProGlyAspTyrGlyGlyProMetPheLeuMetProGlyLeuValIleThrLeuSer 133
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 Qy 134 IleThrGlyAlaLeuAsnThrValLeuThrGluGluHisArgLysGluIleCyAspTyr 153
 Db 243 GTGCTGGAGCACTTAACACTGTCTTCTCATTTGAAACACAGAAAGAGATCCGCCGCTAT 302
 Qy 154 LeuTyrAsnHisGlnAsnLysAspGlyGlyTyrGlyLeuHisGlnGluGlyProSerThr 173
 Db 303 CTTTATATATCAACCAAGATGAAGATGGCGGCTTGACATTTGAAGGATCCAAAGCAC 362
 Qy 174 MetPheGlySerValLeuSerTyrIleThrLeuArgLeuGlyGlyGlyProAsnAsp 193
 Db 363 ATGTTCCGCTCAGCACTGACCTATGTATTGAGATTGCTTGGAGAGGAGCAAGATAGT 422

Qy 194 GlyGlnGlyLysMetGlyLysValAlaArgAspTrpIleLeuGlyHisGlyGlyAlaThrTyr 213
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 Qy 214 IleThrSerTrpGlyLysMetTrpLeuSerValLeuGlyValTyrGluTrpSerGlyAsn 233
 Db 483 ATTAACATCGTGGGGAAGTTTGGCTTCCGTACTAGGTGATTTGATGTGTCTGGTAAAC 542
 Qy 234 AsnProLeuProProGluIleIleTrpLeuLeuProTyrMetLeuProPheHisProGlyArg 253
 Db 543 AACCGGTGCCACCAAGAAATGCTACTGCTCATATCTCCATTTCCACCGAGAGG 602
 Qy 254 MetTrpCyHisCyAspMetValTyrLeuProMetSerTyrLeuTyrGlyLysAspPhe 273
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 Qy 274 ValGlyProIleSerProThrValLeuSerLeuArgLysGlyLeuTyrThrValProTyr 293
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 Qy 294 HisAspIleAspTrpAspGlnAlaArgAsnLeuCyValLysGlyAspLeuTyrTrpPro 313
 Db 723 AGCAAGATTGATTGGAGCAAGGCCCGCAACCTTATGTGCCAAGAAAGATCTGACTAACCA 782
 Qy 314 HisProLeuValGlnAspIleLeuThrAlaSerLeuHisLysPheLeuGluProIleLeu 333
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 Qy 334 MetHisTrpProGlyLysArgLeuArgLysValAlaIleIleSerAlaLeuGluHisIle 353
 Db 843 ATGCATTTGGCTCGGACGACAAATTTGAGGAGAAAGCTCGAAACAGTCATGCAACATGT 902
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 Db 1143 TTGGCTCAACCTTAACTACACACCACTATATCAAGAAATTCACAGGTTTGTATGAC 1202
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 Qy 474 ThrGlyAspHisGlyTyrProIleSerAspCyThrAlaGluGlyLeuLysAlaValLeu 493
 Db 1263 ACTGCTGATCAATGGTTGGCTATATCTGATTCGACAGCTGAAAGGACTTAAGGCTCATTA 1322
 Qy 494 LeuLeuSerLysIleAlaProGluIleValGlyGluProIleAspValLysArgLeuTyr 513
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 Qy 514 AspSerValAsnValIleLeuSerLeuGlnAsnGluAspGlyGlyPheAlaThrTyrGlu 533
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Db		1503	Ggattgatattaccggatgaagtttaagtacatacagaacattccaggccctgcacatttc	1562
Oy		574	Atrylsyleutyprroglvhisargaragluginileglnhisasyilaeaplysalthr	593
Db		1565	AAAAAACTTACCCTGGGCAACCGCAGAAAAGGGTGATTAATTGTTCACGMAACTCC	1622
Oy		594	Thrpheileglulsaleglnalaseraapgysertrpyrglysertppglyvalcys	613
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Oy		614	Phehtirryrglyalatrphelyvalylsglyleuilalaialgilyrserseher	633
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Oy		634	AencysserSerileargylsyalacysgilupheuleuserlyasglneuprosergly	653
Db		1743	AACAGTCCCGCATTTTGAAGAAGCATGCACTTTCTGTTGTCAAAGAACTTCCTCCGCT	1802
Oy		654	giYTPrglygluserytirleusercysgineulysvallyrSerasnleuglulyasn	673
Db		1803	GgTtGGGGAGAAAGCTATTGTTCATCTCAAGCACAGGTTTTACACCAACTCAAGAAC	1862
Oy		674	ArgserHisvalalasnThrclYTrpalawetleualaleuilaaspaliaglylnala	693
Db		1863	CGGCTCCANTGCCGTGAACCTGTGGGGCCATGCGCGCTGATTAAGCGGGCCAGGCC	1922
Oy		694	LysArGaAspserGlnProleuhisArGlaialalyrLeuilaasnserGlnleuglu	713
Db		1923	GAGAGAGATCCAAGCTCTTACACGAGCAGAAAGTTTGATCACTTACATCAAGAG	1982
Oy		714	AepglYaSpPheProGlnglnglnluilemetGlyValPheasnlyAsnCyseMetIethr	733
Db		1983	GACGGAGAAATTCCTCAGCAAGATCATAGAGAGCTTCACAAAGACTGCATGATTAAGC	2042
Oy		734	TyralaalatyraXasnnlePheProileTrpalaleuglyglutryGlnserGlnval	753
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Db		2103	TTG 2105	
RESULT 3				
US-09-419-679-3				
; Sequence 3, Application US/09419679				
; Patent No. 6630617				
; GENERAL INFORMATION:				
; APPLICANT: Falco, S. Carl				
; APPLICANT: Pamodu, Omolayo O.				
; APPLICANT: Hitz, William D.				
; APPLICANT: Kinney, Anthony J.				
; APPLICANT: Rafaleski, Antoni				
; APPLICANT: McGonigle, Brian				
; APPLICANT: Lohman, Karin				
; FILE OF INVENTION: Enzymes Involved In Squelene Metabolism				
; TITLE REFERENCE: BHI13 US NA				
; CURRENT APPLICATION NUMBER: US/09/419,679				
; CURRENT FILING DATE: 1999-10-15				
; EARLIER APPLICATION NUMBER: 60/105,405				
; EARLIER FILING DATE: 1998-10-23				
; NUMBER OF SEQ ID NOS: 16				
; SOFTWARE: Microsoft Office 97				
; SEQ ID NO 3				
; LENGTH: 1882				
; TYPE: DNA				
; ORGANISM: Cyza sativa				
US-09-419-679-3				
Alignment Scores:				
Pred. No.: 1.7e-270 Length: 1882				
Score: 2433.00 Matches: 419				

Percent Similarity:	90.4%	Conservative:	63
Best Local Similarity:	78.6%	Mismatches:	51
Query Match:	58.7%	Indels:	0
DB:	3	Gaps:	0
US-09-419-679-6 (1-757) x US-09-419-679-3 (1-1882)			
QY	222 LeuserValleuglyValTyrGLuTPSerGlyYAsnAsnProLeuProPogluJleTP	241	
DB	15 CTTTGGTGCTGGTGGTATATTGACCTGGTGGCAACACCCAGTGGCACACGAATAATGG	74	
QY	242 LeuLeuProTyrMetLeuProhEnSProGlyATGMetTPCySHisCysAAspMetVal	261	
DB	75 TTGTGGCAATATTTCCTGGCGAATTATCCAGGGCGAATGGGTGATATGGCCGATGGT	134	
QY	262 TyrLeuProMetSerTyrLeuTyrGlyLYsArgPheValGlyProLleSerProThrVal	281	
DB	135 TATTTGGCCATGTGTTCATCTTATGGAAAGAGTTGTGGGCCACATACCAATTTATA	194	
QY	282 LeuSerLeuArgLYsGluLeuTyrThrValProTyrHisAspLleAspTPraaArgLna	301	
DB	195 TTGGAATTTAAGAAAGAACTTACAGAAAGTACCTCAATGAAGATTGATGGCAAGGCT	254	
QY	302 ArgAsnLeuCysAllyLeGluAsnLeuTyrTyrProHisProLeuValGlnAspLleLeu	321	
DB	255 GCGCAATCTAATGGCTAAGGAATCTGATCTATCCATTCATTCGTGCGAGATGATTA	314	
QY	322 TPraLSerLeuHisLYsPheLeuGluProLleLeuMetHisTPRPProGlyLYsArgLeu	341	
DB	315 TGGGCACTCTCACAAATTTGTGTAAACCAAGCATGTGGCGTTGGCGCTGGAAACAAATTG	374	
QY	342 ArgGluLYsAllyLleLeSerAlleuGluHisAlleHisTyrGluAspGluAsnThrArg	361	
DB	375 AGCGAAGAAAGCTTTGGACACTGTGCATGACAGCATATTCAATTATGAAATGAGAACCCGA	434	
QY	362 TyrLleCysLleGlyProValAsnLYsValLleAsnMetLeuCysCysTPRValGluAsp	381	
DB	435 TATATTTTGGCATTTGGTCCAGTAAACAGAGTAAATATCTTGGCTTGGATTTGAAGAT	494	
QY	382 ProAsnSerGlnAllyPheLYsLeuHisLYsLeuProArgLleTyrAspTyrLeuTPRlLea	401	
DB	495 CCAAACTCAGAGGCATTTCAACTCCACATTTCCAAAGAGTCCACATTAACCTATGATTTGCA	554	
QY	402 GluAspGlyMetLYsMetGlnLYTyrAsnGlySerGlnLeuTPraaTPraaAla	422	
DB	555 GAAAGTGGCATGAAATATGACAGGGTTATATGAAAGCCAGCTGTGGACACAGCTTTACA	614	
QY	422 ValGlnAllyLleLleAsnLeuLleGluGluPheGlyProThrLleArgLYsAla	441	
DB	615 GTTCAAGCATATAGTGGCTACTGGCCCTCATTTGAAGAAATTTGGTCTCTTTAAACATGACA	674	
QY	442 HisThrTyrLleLYsAsnSerGlnValleuGluAsnProGlyLYsAsnLeuLYsTPR	461	
DB	675 CATGGCTATATAAAGAAACGACGGTTATCATAGATGCGCTGGAAATCTTATCATAGTGG	734	
QY	462 TyrArgHisLleSerLYsLYsAlaTPRProPheSerThrGlyYAspHisGlyTPRProLle	481	
DB	735 TACCGCCACATATCTAAAGTGCATGGCCCTTTCTACTCGTGATCATGGTTGGCTATA	794	
QY	482 SerAspCysThrAllyGluGlyLeuLYsAlaValLleuLeuLeuSerLYsLleAlaProGlu	501	
DB	795 TCAGATTTCGACGACGAAGGACTTAAAGCGGCAATTATTCGTATCGAAGATTTTCCAGAT	854	
QY	502 LLeValGlyGluProLleAspValLYsArgGlyTyrAspSerValAsnValLleLeuSer	521	
DB	855 ATGTGTGGGGAAGCAGTGGAACTTAAATACCTGTAATGATTCGTCAATTGTGAAGTCA	914	
QY	522 LeuGlnAsnGluAspGlyGlyPheAlaThrTyrGluLeuLYsArgSerTyrAsnTPRLeu	541	
DB	915 TACATGAATGATTAATGGTGGATTTGGCACATATGAACACTACAAGGCTTATGGCTGGCTG	974	
QY	542 GluLleLleAsnProAllyGluThrPheGlyAspLleValLleAspTyrProTyrValGlu	561	

Db 975 GAGCTTATCAATCTCTGACGACCTTTGGGACATTTGATGATTATTCCTTATGTGAA 1034
Qy 562 Cgtrhseralaalaileglnalaualaaserphearglyleuyltrpoglyni valrg 581
Db 1035 TGCACTTGACGACGACATTCAGGCCCTGACAGCATTTAAAMAGCTTACCTGACACGCC 1094
Qy 562 ArggluIuileglnhiacyalileasrlyalaatrtthrpheileglnuylileglnla 601
Db 1095 AAGAGTGAATAGACAACTGTATAGCCAAAGCTGTACTTATTTAGAGGTATTCAAAA 1154
Qy 602 Serarpglysertrpdyrglysertrpdyvalcysphtettrpdyvalatrtphely 621
Db 1155 AGCGATGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1214
Qy 622 VallysglyleuilealaiaaglyarserpheaseranCyserseerleahrglyala 641
Db 1215 GTRAAAGGATTTAGTCTGCTGCTGAGACATTCAAAACAGTCCGACATCAGAAAGCA 1274
Qy 642 Cysglupheleuenserlysglnleuproseryglytrpdygluuserlyleuser 661
Db 1275 TGTCATTTTGTGTGCAAAAGAGCTTCTTCTGAGGCTGGGAGAAAGCTATTTGTCA 1334
Qy 662 Cysgluasnlyvaltyrseranleugluysasnargserhivalvalasnthrgly 681
Db 1335 TCCCAAGATCAGGTTTATACCAATCTCGAAGGAGACGACCTATGCGGTAACTGGT 1394
Qy 682 Trpalemetleuialeuileasrpalaglyglnalaialyargharserserleproleuini 701
Db 1395 TGGGCAATCTAGCTTATTCATTCATGACGAGGAGGAGGAGGAGGAGGAGGAGGAG 1454
Qy 702 Argalaialaalyrleuileasrserglnleugluasrpglyasrphetpoglninglu 721
Db 1455 CGAGGACGCAAGGTTTGTGATCACTTACATCGAAGATGTGAAATTTCCCGACGAAAG 1514
Qy 722 Ilemerglyvalpheasnlyasancysmetlethtrpalaialalytrhrganlelpe 741
Db 1515 ATCATTTGAGTCTTCAACAAACAACTGACATGATGATGATGATGATGATGATGAT 1574
Qy 742 Proiletrpaleuileuglygluyltrglnserglnvalleu 754
Db 1575 CCTATTGGGCTTGGAGATGACGTGCGCGCTCTTG 1613

RESULT 4
US-09-919-039-112
Sequence 112. Application US/09919039
Patent No. 6727066
GENERAL INFORMATION:
APPLICANT: Kaefer, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919, 039
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 112
LENGTH: 4346
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: incycle ID No. 6727066 225080.16
US-09-919-039-112

Alignment Scores:
Pred. No.: 1,03e-179 Length: 4346
Score: 1653.50 Matches: 337
Percent Similarity: 60.2% Conservative: 116
Beet Local Similarity: 44.8% Mismatches: 235
Query Match: 39.9% Indels: 65
DB: 3 Gaps: 15

US-09-419-679-6 (1-757) x US-09-919-039-112 (1-4346)
Qy 17 Leuasnanihsvalglyargglnvaltrpdluhe-----Asrprolyleuenglyser 34
Db 237 CTCACTGCGAGAGGGGGGCGAGAGCTGAGCTTACGTCAGAGAGAGCGGCCGCC 296
Qy 35 ProgluAsrleuengluileglu-----lysalaaarglnAsrphnihsar 50
Db 297 GAGCAGACCGGCTGGAAGCCTTACGCCCTGGGCTGACACCAAGAAATTACTTTAAGAC 356
Qy 51 AsnargphtethnihslynihsersalaAsrleuuewecargmetGlnphealaarglu 70
Db 356 ----- 356
Qy 71 AsnprotharggluvalleuprolyvalglyvalysarplilegluAsrvalthrgln 90
Db 357 -----TTGCCCAAGCC----- 368
Qy 91 GluilevalThnlytrhleuargalavalaserphnihserserThleuglnCyshis 110
Db 369 CACACCGCTTTGAGGGGCTTGAACGAGATGACATTTTACGTGGGCTGACAGCTAG 428
Qy 111 AsrplynihsrtrpoglyAsrtyrglyylprometpheleuemetProglyleuvalile 130
Db 429 GATGGGCACTGAGCGGATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 488
Qy 131 ThrleuserlethrglyalaaleuasnThrvalleuthrgluIuilehialrglylegluile 150
Db 489 ACTTCGACAGTGGCA-----CGCATCTCTGCGACGCGGATACAGAAAGATG 539
Qy 151 CysargtyrleuyltrpAsnhihsleuasnlyasrarglygluyltrpdyglynihsleu 170
Db 540 GTGGGCTACCTGGGCTGAGCTCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 599
Qy 171 Proserthmetpheglseryvalleuserlyrlethrpheleuarglyleugly 190
Db 600 AAGTCACCGTGTGGAGTTCGCTCAACTATGCTCTCAGAAATTCGTGGGTGG 659
Qy 191 ProAsnAsrplyglnlygluemetgluylasrargartrpyleuenglynihsleu 210
Db 660 CCGACGAT-----CTGACCTGTGACGAGCGCGGAACTTTCACAAAGAGTGTGT 713
Qy 211 Alaithrtyrlethsertrpdylysmettrpaleuservalleuglyvaltyrgluutrp 230
Db 714 GCTGTGGCCATCCCTCTGCGGGAAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 773
Qy 231 SerglyAsnAsnProleupProgluiletrpLeuProlyMetleupProphenis 250
Db 774 GAAAGCTCAATACCTGTTCACAGATGTGCTGTTCTGACCTGGGACCGGACGC 833
Qy 251 ProglyargmettrpCyshisCysargmetvaltyrleuprometserlyrleuylgly 270
Db 834 CCTCAGACTGTGGGACCTGCGGAGGAGTGTACTGCTCCATGAGTACTGTACGCGC 893
Qy 271 LyasrghphevalglyProlihserserProthvalleuserleuarglyleuyltrp 290
Db 894 GTTCGGCTGAGTCCCGGAGAGACCGCTGTGCCAGAGCTCCCGGCGGCTGTATGTG 953
Qy 291 ValprotyrhihsarplileAsrtrpAsrplileAsrAsnleuCyalaAsrleuAsrleu 310
Db 954 GAGGACTTGCAGCACTTACCTGTGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1013
Qy 311 TyrttyrProhiAsrleuvalglnAsrileleutrpAlaserlyuhslysrpheleuglu 330
Db 1014 TACAGCCCAACAGCTGGCTGCTCGCGGTATATAGGCTCTCTCAAC----- 1061
Qy 331 ProileuemethttrpoglylylyAsrleuarglygluylasrleuAsrleuAsrleu 350
Db 1062 ---CTGTATGAGACACACACAGTGGCCCACTGCGGAGGAGGAGGAGGAGGAGGAGG 1118
Qy 351 GluhiilehialyrgluAsrlyuAsrleuAsrleuAsrleuAsrleuAsrleuAsrleu 370
Db 1119 GAACACATTTGTGGCGGACGACGATTCACCAAGAGATGACGATGCGGCGGATCTGAAA 1178

371 ValIeuAanMetIeuCySerTrp---ValGIuAepProAanSerGIuAlaIlePheIysIeu 389
1179 ACCATCAACATCTCTGTGGCTGATATGTGACGGGCGGCTCCATGCTCCACAGAG 1238
390 HIsIeuProAgiIeTyAapTyIeuTrpIleAgiuAapGIuMetIyewetGInGIy 409
1239 CATGTCTCAGAAATCCCGAGATATCTCTGATGGGCTTGAACGGCATGAAATGACGGG 1298
410 TyrAanGIySerGIuLeuTrpAapThrAlaPheAlaValGIuAlaIleIle-----Ala 427
1299 ACCAAGCGGCTCAGATCTGGAGACCGCATTCGCAATCCAGGCTCTCTTGAGGGCGGAC 1358
428 SerAanIeuIleGIuPheGIyProThrIleAgiIyAlaIleAaIleThyIleIysAan 447
1359 GGGCACACAGGCGCGAGTTTTCGCTGCGCTCGCAAGGAGCTCATGATCTCTGAGGCTC 1418
448 SerGIuAlaIleuGIuAapCyAepProGIyAapIeuAanIyTrpTyArgHIsIleSerIys 467
1419 TCACAGGTC---CCAGATTAACCTCCGAGCTACAGAAAGTACTACCGCAGATGGCGAAG 1475
468 GIyAlaIleTrpProPheSerThrGIyAapHIsGIyTrpProIleSerAapCyThrAlaGIu 487
1476 GGTGGCTTCTCTTCAAGTACGTGAGCTGCGGCTGATCGTTTCTGACTGACGCGCTGAG 1535
488 GIyIeuIyAlaIleuGIuLeuSerIyIleAlaPheGIuIleValGIyGIuProIle 507
1536 GCTTTGAAGGCTGTCTGCTCTCTGACAGAAAGTCCCATGTACAC---GAGCACTTC 1592
508 AapValIyAargIeuTyAapSerValAanValIleuSerIeuGIuAanGIuAapGIy 527
1593 CCCAGAGAAACGGCTCTGAGATGTCTGTGCTGTGCTGACATAGAAATCCAGATGGA 1652
528 GIyPheAlaIleTrpGIuLeuIyAargSerTyAanTrpIleuGIuIleIleAanProIa 547
1653 GGGTTCGACCTTAAGACCAAGCGTGGGGGCACTTGCTGAGACTCTGAAACCCCTCG 1712
548 GIuThrPheGIyAapIleValIleAapTyProTyValGIuCyThrSerAlaIleIle 567
1713 GAGGCTTCTGGGAGATCATGATTAATTAACCTTAATGTGAGAGTCACTTCAAGCCGTATG 1772
568 GIuAlaIleuAaIleSerPheAgiIyIleuTyAargProGIyHIsAargAgiuGIuIleGIuHIs 587
1773 CAGGCGCTTAAGTATTCACAAAGCGTTTCCGAGGACAGGGGACGCGAGATCCGGGAG 1832
588 CyIleAapIyAlaIleThyPheIleGIuIyIleGIuAlaIleSerAapGIySerTrpTy 607
1833 ACCCTCAGCGAGGCTTGAAGTCTGTGCGCGGACAGAGGCGGATGCGCTCCGCGGAA 1892
608 GIySerTrpGIyValCyAepThrTyGIyAlaIleTrpPheGIyValIyGIuLeuIleAla 627
1893 GGGCTCTGGAGAGTTTGCTTCACTTACCGACACTGTGTGGCTGGAGGCGCTTGGCGCTGT 1952
628 AlaGIyAargSerPheSerAan-----CySerSerIleAargIyAlaCyGIuIlePhe 644
1953 ATGGGGCAGACCTACCGAGATGGAGCTGCTGAGAGGTCCTCCCGGCGCTGTGACTTC 2012
645 IeuIeuSerIyGIuIleuProSerGIyGIyTrpGIyGIuSerTyTrIeuSerCyGIuIleAan 664
2013 CTGCTGTCCCGCAGATGCGAGACGCGAGGCTGGGGGAGAGCTTTGACTCTCTGCGAGAG 2072
665 IyAaIleValIySerAanIleuGIuGIyAanAargSerHIsAlaIleAanThyGIyTrpAlaMet 684
2073 CGGCGCTTAT-----TTCAGAGAGTCCCAAGTCCAGATTCATTAACATGCTGGGCGCATG 2126
685 IeuAlaIleuIleAapAlaGIyGIuAlaIyAargAapSerGIuProIeuHIsAargAlaIle 704
2127 ATGGGGCTGATGGCGCTTCGAGATCTGACATCGAGCGCCAG-----GAGAGAGGATC 2180
705 AlaTyTrIeuIleAanSerGIuLeuGIuAapGIyAapPheProGIuIleGIuIleMetGIy 724
2181 CGGTGTCTAATTGAGAAACAGCTCCCAATGCGAGCTGCGCGCAGAGAAATATGCTGTGG 2240

725 ValPheAanIyAaIleuCyMetIleThyTrpAlaIleTyArgAanIlePheProIleTrp 744
2241 GTCTTCAACAGTCTGTGGCATCTCTTACACAGAGCTTACAGAAATCTTCCCATCTCG 2300
745 AlaIeuGIyGIuTrpGIuIleuSerGIuValIleuGIuSerAarg 757
2301 GCGCTCGGCGCGCTTC---TCCAGCTGTACCTGAGAGA 2336
RESULT 5
US-09-815-048-1
; Sequence 1, Application US/09815048
; Patent No. 6737261
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: C1001180
; CURRENT APPLICATION NUMBER: US/09/815,048
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ. ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ. ID NO 1
; LENGTH: 4239
; TYPE: DNA
; ORGANISM: Human
US-09-815-048-1
Alignment Scores:
Pred. No.: 3,37e-173 Length: 4239
Score: 1597.00 Matches: 329
Percent Similarity: 59.1% Conservative: 116
Best Local Similarity: 43.7% Mismatches: 232
Query Match: 38.5% Indels: 76
Gaps: 16
US-09-419-679-6 (1-757) x US-09-815-048-1 (1-4239)
QY 17 IeuAanAanHIsValGIyAargGIuValTrpGIuIle-----AapProIyIleuGIySer 34
DB 112 CTCAACTGCGAGAGGCGCGGAGCGTGAACCTTACCTGACAGACGAGCGGCGCGC 171
QY 35 ProGIuAapIleuGIuIleGIu-----IyAaIleAargIuAanPheHIsAap 50
DB 172 GAGGACACCGGCTGGAAGCTTACGCGCTGGGCTGAGACACCAAGATTTACTTTAAGAC 231
QY 51 AaAargPheThrHIsIyHIsSerAlaAapIleuIleAargMetGIuIleAargGIu 70
DB 231 ----- 231
QY 71 AaAapThrAargGIuValIeuProIyValGIyValIyAapIleGIuAapValThrGIu 90
DB 232 -----TTGCCCAAGCC----- 243
QY 91 GIuIleValIleThyIleAargAargAlaIleSerPheHIsSerThrIleuGIuIleHIs 110
DB 244 CACACCGGCTTGAAGGCGCTGACAGGAGATGACATTTAATCGGGGCTGACAGGCTGAG 303
QY 111 AapGIyHIsTrpProGIyAapTyArgIyGIyProAapPheIleuMetProGIyIleuValIle 130
DB 304 GATGGGACATGAGAGGCTGATTAATGTGGCCACTTTCTCTCTGCGCAGGCGCTCTGATC 363
QY 131 ThrIeuSerIleThyGIyAlaIleuAanThyValIeuThrGIuGIuHIsAargIyIleGIuIle 150
DB 364 ACTTGCCACGTGCA-----CGCATCCCTCTGCGACCGGATTCAGAGAAAGATTT 414
QY 151 CyAargTyTrIeuTyAanHIsGIuAanIyAapGIyGIyTrpGIyIleHIsIleGIuGIy 170
DB 415 GTGGGATCTG-----CGGCACTTGAGGAT 441
QY 171 ProSerThrMetPheGIySerValIeuSerTyIleThrIleuAargIleuGIyGIuGIy 190
DB 442 AAGTCCACCGTGTGGAGTCTGCGGCTCAACTATGTGTCTCAGAAATTTGGGTTGGG 501

QY 191 ProAnaMetGlyGlnGlyGlnMetGlyValArgArgProTyrIleLeuGlyHisGlyGly 210
 DB CCGTGAACGAT-----CCTGACCTGGTACGAGCCCGGACCATCTTCACAAAGAGTGGT 555
 QY 211 AlaThrTyrIleThrSerTyrGlyMetTyrPheSerValLeuGlyValTyrGluTyr 230
 DB 556 GGTGGGCGCATCCCTCCCTGGGGGAGTTCGTGGCTGGCTGCTCCGTGAATTTTACAGCTGG 615
 QY 231 SerGlyAsnAsnProLeuProProGluIleTyrPheLeuProTyrMetLeuProPheHis 250
 DB 616 GAAGGCTCATATACCTGTTCCTCCAGAGATGGCTGTTCCTGACCTGGGACCCGAGAC 675
 QY 251 ProGlyArgMetTyrCysHisCysArgMetValTyrLeuProMetSerTyrLeuTyrGly 270
 DB 676 CCTCCACACTCTGGGGTCCAGCTGGCCGAGGTGTACTCCCATGAGTACTGCTCAAGCC 735
 QY 271 LysArgPheValGlyProIleSerProThrValLeuSerLeuArgGlyGlyLeuTyrThr 290
 DB 736 GTTCGGCTGATGGCCCGGAGAACCCGCTGGTCCAGAGCTCCGACAGAGCTCATATGG 795
 QY 291 ValProTyrHisAsnIleAsnTyrPheArgIleAlaArgAsnLeuCysAlaYsgIleAsn 310
 DB 796 GAGGACTGGCCAGCATATGCTGGCTGGCCGAGAGAACAGCTGGCCCCACAGACTG 855
 QY 311 TyrTyrProHisProLeuValGlnAsnIleLeuTyrAlaSerLeuHisValPheLeuGln 330
 DB 856 TACAGCCCGCACAGCTGGCTGCTCCGGGTGTATGCGCTCTCAAC----- 903
 QY 331 ProIleLeuMetHisTyrProGlyLysArgLeuArgGlyValAlaIleLeuSerAlaLeu 350
 DB 904 ---CTGTATGAGCAGCAGCAGCAGTGGCCACTGGCAGGCGGCTGGCAGAGCTGTAT 960
 QY 351 GlnHisIleHisTyrGlnArgIleAsnThrArgTyrIleCysIleGlyProValAsnLys 370
 DB 961 GAACACATTTGTGGCCGACGACCGATTCACCAAGAGATTCAGCATCGCCCGCATCTGAAA 1020
 QY 371 ValLeuAsnMetLeuCysCysTyr---ValGlnAsnProAsnSerGlnAlaPheLysLeu 389
 DB 1021 ACCATCAACATGTTGTGGCTGGTGTATGTGAGGGGCGCGCTCCACTGCTTCCAGGAG 1080
 QY 390 HisLeuProArgIleTyrArgTyrLeuTyrIleAlaGlnAsnArgLysMetGlnGly 409
 DB 1081 CATGTCTCCAGAAATCCCGGACTATCTGTGATGGCGCTTGCACGAGTGAAGACAGGGC 1140
 QY 410 TyrAsnGlySerGlnLeuTyrAsnThrAlaPheAlaValGlnAlaIleIle-----Ala 427
 DB 1141 ACCAAGCGCTCACAGATCTGGACACCGCATTCGACCATCGAGCTTGGAGCGGGC 1200
 QY 428 SerAsnMetLeuIleGluGluPheGlyProThrIleArgLysAlaHisThrTyrIleLysAsn 447
 DB 1201 GGGGACACAGAGCCCGAGTTTGTGCTGCTGCTGACAGAGGCTCATAGTTCTCGAGGCTC 1260
 QY 448 SerGlnValLeuGlnAsnProGlyAsnProGlyAsnLeuAsnLysTyrTyrArgHisIleSerLys 467
 DB 1261 TCACAGGCT---CCAGTAAACCTCCCGGACTACAGAGAACTACACCGCAGATGGCAG 1317
 QY 468 GlyAlaTyrProPheSerThrGlyAsnHisGlyTyrProIleSerAsnProValAlaGlu 487
 DB 1318 GGTGGCTTCTCTTCAGTACGCTGGACTGGCTGGCTGGATCTGCTTGTGCTCAGCGGCTGAG 1377
 QY 488 GlyLeuValAlaValLeuLeuLeuSerLysIleAlaProGluIleValGlyGluProIle 507
 DB 1378 GCTTGAAGGCTGTGCTGCTCTCCAGAGAAAGTGTCCCATGTCAAC---GAGCAATC 1434
 QY 508 AsnValLysArgLeuTyrAsnSerValAsnValIleLeuSerLeuGlnAsnGluAsnGly 527
 DB 1435 CCCAGAGAACGGCTCTCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1494
 QY 528 GlyPheAlaThrTyrGlyLeuLeuValArgSerTyrAsnThrLeuGluIleIleAsnProAla 547
 DB 1495 GGGTTCGACACTATGAGACCAACGCTGGGGGCACTTGTGAGCTGTGAACCCCTCG 1554

QY 548 GluThrPheGlyAsnIleValIleAsnTyrProTyrValGlnCysThrSerAlaIle 567
 DB 1555 GAGGTCTTCGGAGACATATGATTTGATTCACACCTATGTGAGTGCACCTGAGCCGTGATG 1614
 QY 568 GlnAlaLeuAlaSerPheArgLysLeuTyrProGlyHisArgArgGluGluIleGlnHis 587
 DB 1615 CAGGCGCTTAAGTATTTCCACAGAGGCTTCCCGGAGCAGAGGCGAGCGAGATCCGGAG 1674
 QY 588 CysIleAsnLysAlaThrThrPheIleGluLysIleGlnAlaSerAsnGlySerTyrThr 607
 DB 1675 ACCCTCAGCAGAGGCTTGAAGTGTGGCGGAGCAGAGGCGAGATGGCTCCCTGGAAA 1734
 QY 608 GlySerTyrGlyValCysPheThrTyrGlyAlaTyrPheGlyValIleGlyLeuIleAla 627
 DB 1735 GGTCTCGGAGGTTCCTTCACTTACGACCTGTTGGCTTGGCTTGGAGCCCTGGCTGT 1794
 QY 628 AlaGlyArgSerPheSerAsn-----CysSerSerIleArgLysAlaCysGluPhe 644
 DB 1795 ATGGGGCAGACTTACCGAGATGGAGCTGCTGTGAGAGTCTCCGGGCTGTGACTTC 1854
 QY 645 LeuLeuSerLysGlnLeuProSerGlyGlyTyrGlyGlySerTyrLeuSerCysGlnAsn 664
 DB 1855 CTGCTGTCCCGCAGATGGCAGACGAGGCTGGGGGAGACTTGAAGTCTGCGAGAG 1914
 QY 665 LysValTyrSerAsnLeuGluGlyAsnArgSerHisValAlaAsnThrGlyTyrAlaMet 684
 DB 1915 CGGCGTTAT-----GTGAGAGTCCAGTCCAGATTCACACACATGCTGGCCATG 1968
 QY 685 LeuAlaLeuIleAsnAlaGlyGlnAlaLysArgAsnSerGlnProLeuHisArgAlaAla 704
 DB 1969 ATGGGCTGATGATCCGCTTCCGATCTGCAATCAGAGGCCAG-----GAGAGAGAGTC 2022
 QY 705 AlaTyrLeuIleAsnSerGlnLeuGluAsnArgIleAsnPheProGlnGlnIleMetGly 724
 DB 2023 CGGTGCTACTGAGAAACAGCTCCCAATGCGAGCTGGCCCGCAGAGAAACATTTGCTGG 2082
 QY 725 ValPheAsnLysAsnCysMetIleThrTyrAlaAlaTyrArgAsnIlePheProIleTyr 744
 DB 2083 GTCCTCAACAAATCTGTCGCTTCCTTACAGAGAGTACAGAAACATTTCCCATCTGG 2142
 QY 745 AlaLeuGlyGlyTyrGlnSerGlnValLeuGlnSerArg 757
 DB 2143 GCCCTGGCGGCTTC---TCCAGCTGTACCTGAGAGA 2178
 RESULT 6
 US-09-419-679-7
 ; Sequence 7, Application US/09419679
 ; Patent No. 6630617
 ; GENERAL INFORMATION:
 ; APPLICANT: Falco, S. Carl
 ; APPLICANT: Famodu, Omolayo O.
 ; APPLICANT: Hite, William D.
 ; APPLICANT: Kinney, Anthony J.
 ; APPLICANT: Rafaleki, Antoni
 ; APPLICANT: McGonigle, Brian
 ; APPLICANT: Lohman, Karin
 ; TITLE OF INVENTION: Enzymes Involved in Squalene Metabolism
 ; FILE REFERENCE: BBI113 US NA
 ; CURRENT APPLICATION NUMBER: US/09/419,679
 ; EARLIER APPLICATION NUMBER: 60/105,405
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 7
 ; LENGTH: 1300
 ; TYPE: DNA
 ; ORGANISM: Trilicium aestivum
 ; US-09-419-679-7
 Alignment Scores: 3,66e-156 Length: 1300
 Pred. No.: 1442.00 Matches: 257
 Score:

Percent Similarity: 88.54 Conservative: 42
Best Local Similarity: 76.04 Mismatches: 39
Query Match: 34.84 Indels: 0
DB: 3 Gaps: 0

US-09-419-679-6 (1-757) x US-09-419-679-7 (1-1300)

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OY 417 AEPTRAlaphaAlValGlInAllelleAlaSerAenLeuileGluGluPheGlyPro 436
DB 8 GACACAGCTTTTGCAAGTTCAAGCTTTCGGCCACTGACCTCATTTGAAGAGTTGCTCC 67
OY 437 ThrileArgLysAlaHisThrTyrlleLysAenSergInValleGluAerCyapProGly 456
DB 68 ACTCTTAAGCTGGCAGCATGATTTTATTAAGAACTCTCAGGTTGTGAGTACGCTCGA 127
OY 457 AspleuAenLysTrpTyrlArgHisIleSerLysGlyAlaTrpProPheSerThrGlyAer 476
DB 128 GATCTGAGTTACTGTGATCCGTCACATATCTMAAGGTGATGGCCCTTTTCTACAGCTPAT 187
OY 477 HisGlyTrpProLleSerAerCyapThrAlaGluGlyLeuLysAlaValleuLeuLeuSer 496
DB 188 CATGGTTGGCTTATATTCAGATTGCTGACCTGACAGAGAACTMAAGCCTCATTTGCTTACA 247
OY 497 LysAlaAlaProGluLleValGlyLysProLleAerValLysArgLeuTyrlAerSerVal 516
DB 248 AAGATTCTCCAGAAATTTGGGGCGAATCGGTGAAGTTAACAGACTATATGATGCTGTC 307
OY 517 AenValIleleuSerleuGlnAenGluAerGlyGlyPheAlaThrTyrlGluLeuLysArg 536
DB 308 AATGTGTGATGTCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 367
OY 537 SerTyrlAenTrpLeuGluLlelleAenProAlaGluTrpPheGlyAerPleValIleAer 556
DB 368 TTTTATGCTGCTGCTGCTGCTGCTTATCACTCCGAGAACTTCGAGAAATTTGATTTGAT 427
OY 557 TyrlProTyrlValGluCyerThrSerAlaAlaIleGlnAlaLeuAlaSerPheArgLysLeu 576
DB 428 TACCGGTATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 487
OY 577 TyrlProGlyHisArgArgGluGluLleGlnHisCyrlleAerLysAlaThrThrPheIle 596
DB 488 TATCTGTGGGACCCGAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 547
OY 597 GluLysIleGlnAlaSerAerPglYserTrpTyrlGlySerTrpGlyValCyepheThrTyrl 616
DB 548 GAGAGCATCCAAAGAAAGATGCTTCAAGTATGCTCTGGGCTGTGTGCTTCACTCAT 607
OY 617 GlyAlaTrpPheGlyValLysGlyLeuIleAlaIleArgSerPheSerAenCyapSer 636
DB 608 GGCACATGCTTGGAGTGAAGGGGCTACTAGCTGAGAGTGAAGAACTTCAGAGCAGTCT 667
OY 637 SerIleArgLysValCyegluPheLeuLeuSerLysGlnLeuProSergLysGlyTrpGly 656
DB 668 GCAACTCAAAAGGCACTGTGATCTTGTGATGATGATGATGATGATGATGATGATGATGAT 727
OY 657 GluSerTyrlleuSerCyegluAenLysValTyrlSerAenLeuGluGlyAenArgSerHis 676
DB 728 GAAAGCTATCTGTCTCACTCAAGATCAAGTTTACACCATCTTGAAGGGAAGATCTCAT 787
OY 677 ValValAenThrGlyTrpAlaMetLeuAlaLeuIleAerAlaGlyGlnAlaLysArgAer 696
DB 788 GCTGTCAACACTGGCTGGGCCATGCTGACTTAAATTGACGAGGACAGGCTGACAGAGAC 847
OY 697 SerGlnProLeuHisArgAlaAlaAlaTyrlleuIleAenSergInleuGluAerGlyAer 716
DB 848 CCGAGCCCTCTGCTGATCGAGCAGCGAAGTTTGTGATTAACCTTACAGAGATGGGAAA 907
OY 717 PheProGlnGlnGluIleMetGlyValPheAenLysAenCyapMetIleThrTyrlAlaAla 736
DB 908 TTTCTCTGACAGAGATCATGGAGTCTTCAACAAAGAACTGCAATGATGATGATGATGATGAT 967
OY 737 TyrlArgAenIlePheProLleTrpAlaLeuGlyGlyTyrlGlnSergInValleu 754
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DB 968 TATCGAACAATCTTCCCTATCTGGGCGCTTGGCGAGTACCGCTCGGGTCTG 1021
RESULT 7
US-09-614-221A-308
; Sequence 308, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
; APPLICANT: Karunananda, Balasubojini
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Kishore, Ganesh M.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
; FILE REFERENCE: 16516.075
; CURRENT APPLICATION NUMBER: US/09/614,221A
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/142,981
; NUMBER OF SEQ ID NOS: 626
; SEQ ID NO 308
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-614-221A-308
Alignment Scores:
Pred. No.: 1,436-136      Length: 2196
Score: 1276.00      Matches: 303
Percent Similarity: 53.94      Conservative: 114
Best Local Similarity: 39.14      Mismatches: 263
Query Match: 30.84      Indels: 94
DB: 3      Gaps: 23
US-09-419-679-6 (1-757) x US-09-614-221A-308 (1-2196)
OY 1 MetTrpLysLeuLysPheAlaGluGlyGlyAenProTrpLeuAgtTrleuAenHis 20
DB 52 CTTGAGAGCTGAGA-----ACTGATAG 75
OY 21 ValGlyArgGlnValTrpGluPhe-----AerProLysLeu 32
DB 76 CTAGGCGGAGAAAGCTGGGAAATATTTAACCCCTGACAGACCGGAAAGACCCATGCTC 135
OY 33 GlySerProGlnAerLeuGluLleGlyLysAlaArgGlnAenPheIleAerAerAer 52
DB 136 ACTTCAAGGAGGCTGCTTCAAGATCCCAATTTCTCAAGCT---CATCGAAGAGA 192
OY 53 PheThrHisLysHisSerAlaAerLeuMetArgMetGlnPheAlaArgGluAerPro 72
DB 193 -----AATMAAGCATTCACCGAGATTT----- 213
OY 73 ThrArgGluValleuProLysValGlyValLysAerPleGluAerValThrGlnGluIle 92
DB 214 -----TCA 216
OY 93 ValThrLysTrleuAerGArgAlaValSerPheHisSerThrLeuGlnCyapHisAer 111
DB 217 GCTTCGATGGGTGATCAATAGTGCATCTTTTCAAGCTTCAAGGCTTCAAGGCTGATGCA 276
OY 112 GlyHisTrpProGlyAerTyrlGlyLysProMetPheLeuMetProGlyLeuValIleThr 131
DB 277 GGTATTTTTCCTGTCAATATTAAGAACCCATGTTTCAATGATGATGATGATGATGATGATGAT 336
OY 132 LeuSerIleThrGlyAlaLeuAerThrValleuThrGluGluHisArgLysGluIleCys 151
DB 337 AACTATATCGCGGAT-----ATTGAATTTCTGAGCTGAGAGATGAAATTATTT 387
OY 152 ArgTyrlleuTyrlAenHisGlnAenLys-----AerGlyGlyTrpGlyLeuHisIleGluGly 170
DB 388 AGATATCATGTCATATACAGCAGCATCGGTTGATGCTGGCTGGGCTGATATTCGTTGAC 447
OY 171 ProSerThrMetPheGlySerValleuSerTyrlleThrleuAerLeuGlyGlyGly 190
DB 448 AATTCACCGGTGTTGGTACAGTATGAACTATGATATCTTACGTTATTTGGGTCTA--- 504
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QY 191 ProAenAerGlyGlnGlyGluGluValAaAaAerTrpIleLeuGlyHisGlyGly 210
 DB 505 CCCAAGGAC---CACCCGGTTGGCCCAAGGACAAAGACACATTTGTAAGTTAGCGCGGT 561
 QY 211 AlaTrpTrpIleThSerTrpGlyGluMetTrpLeuSerValLeuGlyValTrpGluTrp 230
 DB 562 GGTATGTGATCCCTCACTGAGGGGAAAATTTGGCTAAGTCACTAACTGTATAAATGG 621
 QY 231 SerGlyAenAerProLeuProProGluIleTrpLeuLeuProTrpMetLeuProPheHis 250
 DB 622 GAAGGTGAGACCCCTGCCCCCTCTCAAACTGTTACTTCATTCATTCAGTCCGACAT 681
 QY 251 ProGlyAerMetTrpCysHisCysAerMetValTrpLeuProMetSerTrpLeuTrpGly 270
 DB 662 CCGGGAGATGGTGGGTTCACTAGAGGTGTTTACATTCGCGGTGAGTACCTGTGCATGG 741
 QY 271 LysAerGlyValGlyProIleSerProTrpValLeuSerLeuTrpGlyGluLeuTrpTrp 290
 DB 742 GTCAATTTTCTTGGCCCAATGACTCTCTTCTTGAAAGAACTGAGGAATGAAATTTTACCT 801
 QY 291 ValProTrpHisAerTrpAerTrpAerGlnAlaAerAerLeuCysAlaValGluAerLeu 310
 DB 802 AAACCGTTTGACAAAGTAACTTCTCAAAACGGAATACCGTATGAGTACAGCTA 861
 QY 311 TyrTrpProHisProLeuValGlnAerIleLeuTrpAlaSerLeuHisLysPheLeuGlu 330
 DB 862 TATTACCCCATTTACTTACTTATGATATTTGGC---AACAGCTTGTAGATTTTTCGAA 918
 QY 331 ProIleLeuMetHisTrpProGlyLysAerGluValGluValAlaIleLeuSer----- 348
 DB 919 -----AAATACCTAAAGAAACCGGTTCCTTACTTACTCTTATCC 954
 QY 349 -----AlaLeuGlnHisIleHisLysTrpGluAerGluAerHisTrpTrpIleCysIle 365
 DB 955 AAGAAAGAGGTTTATATCTTAACTCAAAACGGAATTAACGATATCTGATTCCTTGTTATA 1014
 QY 366 GlyProValAerLysValLeuAerMetLeuCysLysTrpValGluAer---ProAenSer 384
 DB 1015 GCACCTGTTTACACAGCGCTTTGGCAGCTTGTCACTTATTAAGAAAGCGGTAGACTGG 1074
 QY 385 GlnAlaPheLysLeuHisLysLeuProAerGlyLysTrpAerTrpLeuTrpIleAlaGluAerGly 404
 DB 1075 GAAGCGTTCAGAGCGTCCCAATATAGTTCAGAAAGTCACTTGTTCATGCTCCACAGCGGT 1134
 QY 405 MetLysMetGlnGlyLysAerGlySerGlnLeuTrpAerHisAlaPheAlaValGlnAla 424
 DB 1135 ATGACCATTAATGGGAACAAATGGTGTGCAAACTGGAGATTGTGCTTGCATTTCAATAC 1194
 QY 425 IleIleAlaSerAerLeuIleGlu-----GluPheGlyProTrpIleAerGlyAlaHis 442
 DB 1195 TTTTGTGTCGACAGCGCTCGCAAAAGAACTGAAATTCATTAACAATTTGCTGTGCTAT 1254
 QY 443 ThrTrpIleLysAerGlnValLeuGluAerCys---ProGlyAerLeuAerLysTrp 461
 DB 1255 AAATCTGTGTGATGTCATTAATTTGACACCGAGTGCCTTCAGATAGT----- 1302
 QY 462 TyrAerHisIleSerLysGlyAlaTrpProPheSerHisLysAerHisGlyTrpProIle 481
 DB 1303 TATAGGATTAAGAAAGGGGCGTGTGGGCTTCTCAACAAACACAGGGCTTATACAGTG 1362
 QY 482 SerAerCysPheHisAlaGluGlyLeuLysValLeuLeuLeu-----SerLysIleAla 499
 DB 1363 GCAGATTGCACTGCAAGAAACATTAAGCCATCATCATCTGTAAGAAAACCTCCCGCTTTT 1422
 QY 500 ProGluIleValGlyGluProIleAerValLysAerGlyLysTrpAerSerValAerValIle 519
 DB 1423 AGTGA---GTACACCATATGATTAAGAGTAAAGCTTATTTGAAGCATTTGATGTGTTA 1479
 QY 520 LeuSerLeuGlnHis-----GluAerGlyLysPheAlaTrpTrpGluLeuLys 535
 DB 1480 TTGAACCTTACAAACATCGGATCTTTGAAATATGTTCTTTGCAACCTTAAGAAAATATC 1539

QY 536 ArgSerTrpAerTrpLeuGluIleIleAerProAlaGluTrpPheGlyAerPheValIle 555
 DB 1540 AAGGCCCACTAGCAATGAAGAAACCTTGAAATCTCTGTGAAGTTTGGTGAATATATGTA 1599
 QY 556 AspTrpProTrpValGluCysThrSerAlaAlaIleGlnAlaLeuAlaSerPheArgLys 575
 DB 1600 GAATCCCATACGTGGATGATGATGATTCATCCGTTCTGGGGTTCACATATTTTCACAAG 1659
 QY 576 LeuTrpProGlyHisAerArgGluGluIleGlnHisCysIleAerValAlaThrTrpPhe 595
 DB 1660 ---TACTTCGATATAGGAAAGAGAAATAGCATACACCATCAGAAATGCCATCGAATTC 1716
 QY 596 IleGluLysIleGlnAlaSerAerPheGlySerTrpTrpGlySerTrpGlyValCysPheThr 615
 DB 1717 ATAAAAAATTCATTAACCAATGAAGATGAGTGGATGAGAGCTGGGGATTTGTTTACA 1776
 QY 616 TrpGlyAlaTrpPheGlyValAlaGlyLeuIleAlaAlaGlyAerSerPheSerAerCys 635
 DB 1777 TATGCCGATGTTTGCATTTGAGAGCATTTTACACACCGTGGGGAGACCTATGAGAAATCC 1836
 QY 636 SerSerIleAerGlyValCysGluPheLeuSerLysGlnLeuProSerGlyGlyTrp 655
 DB 1837 TCACGGGTAAAGAAAGTTGCGACTTCTTGTGACGTAAACGATGAGATGCGGTGG 1896
 QY 656 GlyGluSerTrpLysLeuSerCysGlnHisLysValTrpSerAerLeuGluGlyAerHisSer 675
 DB 1897 GGGGAATCAATGAATGCC-----AGTAATTAACATGATTATGTGATAGTAAATATCG 1950
 QY 676 HisValAlaAerHisGlyTrpAlaMetLeuAlaLeuIleAerAlaGlyGlnAlaLysArg 695
 DB 1951 CTAGTCGTTCAAAACCGCATGGCGCTTAATGACATCTTTTGGCGAATATCTTAATA 2010
 QY 696 AspSerGlnProLeuHisArgAlaAlaAlaTrpLeuIleAerSerGlnLeuGluAerGly 715
 DB 2011 -----GAAGTCATGACCGCGGTATGACTTGTAAATAAATGACAGAAAGAAATCCGGG 2064
 QY 716 AspPheProGlnGluIleMetGlyValPheAerLysAerCysMetIleThrTrpAla 735
 DB 2065 GAATGAAATTTGAAAGTGTAGAGGTGTTTCAACCACTTGTGCAATTAATTAACCA 2124
 QY 736 AlaTrpAerAerHisLysPheProIleTrpAlaLeuGlyGluTrp 749
 DB 2125 AGTATCGATTTCTTATTCCTTATTAAGCATTAAGGATATGATAC 2166
 DB: 3

RESULT 8
 US-09-248-796A-3811
 ; Sequence 3811, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Kelch Weinstock et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248,796A
 ; PRIOR FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,725
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096,409
 ; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208
 ; SEQ ID NO 3811
 ; LENGTH: 747
 ; TYPE: DNA
 ; ORGANISM: Candida albicans
 US-09-248-796A-3811

Alignment Scores:
 Pred. No.: 1,78e-36 Length: 747
 Score: 403.50 Matches: 84
 Percent Similarity: 53.0% Conservative: 30
 Best Local Similarity: 39.1% Mismatches: 76
 Query Match: 9.7% Indels: 25
 DB: 3 Gaps: 6


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; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085,500-US
; CURRENT FILING DATE: 2001-10-05
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1079
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-1079

Alignment Scores:
Pred. No.: 2,5e-27 Length: 1512
Score: 329.00 Matches: 132
Percent Similarity: 39.24 Conservative: 95
Best Local Similarity: 22.84 Mismatches: 246
Query Match: 7.9% Indels: 106
DB: 5 Gaps: 21

US-09-419-679-6 (1-757) x US-09-974-300-1079 (1-1512)
Oy 82 VallyuAARlIeGluAARValThrGluGluValThrLysThrLeuAARgAlaVal 101
Db 6 CTAGAAGACGTGAAGCTTTCAGGCAAAAGCGTCGAGAGCTTCAAAACGA----- 59
Oy 102 SerpheniSerThrLeuGlnCyshIaARgLyhiStrProGluAARLyrgLyPro 121
Db 60 -----CAAGATCTGATGGTTCGCGGCTTTGTTTGAAGGCC 101
Oy 122 MetRheleuMetProGluLeuValIleThriLeuSerIleThriValLeuAanThraI 141
Db 102 GTGATGACGACGAGTTTTCATCTGATGCTGACATCACTCGGCGATCAGGACTCTCT 161
Oy 142 LeuThriGluGlnIleAARgLyLeuCyAARgLyLeuThraAanIleGlnAanLyAAR 161
Db 162 CTCATC-----GCAAGCTTGTGTCAGCAAGATCCGTTCAAGCGCAAGCAAGAC 209
Oy 162 GlyLyTrpGlyLeuGlnIleGluLyProSerThrMetRheGlySerValLeuSerTy 181
Db 210 GCGCGGTTCCGAACTC-----CCGATGAAGAAGCAGCAATCTGACCCGACGA 260
Oy 182 IleThr-----LeuAARgLeuGlnLyGluLyProAanAARgLyGlnGly----GluMet 198
Db 261 GTCCAGGCGCTATACCGGAATGCTGGCTTCGCGGCTCTATGACCGGAAAGCTCCGCAATG 320
Oy 199 GlnLyValAARgAARTrpIleLeuGlnIleGlyGlyAlaThraThraIleThSerTrpGly 218
Db 321 CAGAAAGCCGAAGCTTTATTATTAAGACCGAGCGGATTTGAAGGGCGCTCATTTATGACG 380
Oy 219 LysMetTrpLeuSerValLeuGlyValLyTrpSerGlyAanAanProLeuProPro 238
Db 381 AAGTGAATGCTCGCGCAACCGCTGTATCCATGAGCGG---AGAGCTTATATTCGCGTC 437
Oy 239 GluIleTrpLeuLeuProTyMetLeuProPhehIaSProGlyAARMetTrpCyhiAcy 258
Db 438 TCGTTTGTCTGATCCGCTCTATTTCGCGTGCATTTTACATTTACATTCAGCAATACGCA 497
Oy 259 ArgMetValLyLeuProMetSerTyLeuTyrgLyAARgPhe----- 273
Db 498 AGAATTCATTTTGTCCCATGCGCATTCAGCTTATCGCGCATTTCTTTAAAAAACACAC 557
Oy 274 ---ValGlyProIleSerProThraValLeuSerIleAARgLyGlnLeuTyThraValPro 292
Db 558 CAATCGGC-----TCGCTTCGCAACCTGATGAAGCCATGCA 596
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Oy 293 TyThiAARlIeAARTrpAARgAlaAARgAanLeuCyValLyGlnAARLeuTyTh 312
Db 597 AAAAACCTCTGAAATGCTGAAATCCG-----GCTTGAACGAAGAACTTCTAT 650
Oy 313 ProhIaARLeuValGlnAARlIeLeuThraIaSerLeuGlnIleThraPheLeuGlnProIle 332
Db 651 TCTTTC-----AATCTGCAATGGAACAGCTC-----TTTCATAGCCGCGCT 692
Oy 333 LeuMetIaStrProGlyLyAARgLeuAARgGlnLyValIleIleSerAlaLeuGlnIle 352
Db 693 TACGTCAATAGCTCGGATTTGAGCGCGGCAAAATATATGCTGCAACAGATC----- 746
Oy 353 IlehiTyrgLeuAARgAanThraGTrIleCyhiIleGlyProValAanLyValLeu 372
Db 747 -----GAAGAAGCGAAGCGCTTATACAGCTATGCGAGCGGACCATTTGATGATT 797
Oy 373 AAnMetLeuCyAARTrpValGluAARProAanSerGluAARhLeuLyLeuLeuPro 392
Db 798 TACAGCGCTGTCGATGGGAATGTATTAACCGCCCGCTTGCATTAAGACAGTCAGC 857
Oy 393 ArgIleTyraARTrpLeu---TrpIleAAGluAARlIeMetLyMetGlnLyThraAn 411
Db 858 GGAATCAAAAGCTTATTTATCATCATGCGGAAGAGAGGCGCCATTTGAAAC--TCA 914
Oy 412 GlySerGlnLeuTrpAARThraIaPheAlaValGlnAlaIleIleAaSerAanLeuIle 431
Db 915 ACTTCACCGCTGGATACCGCCCTCATCAGCTATGCAAGATCCGAGAGTCCCT 974
Oy 432 GluGlnPheGlyProThr-----IleArg 439
Db 975 GAACAAATCTTTCACATCTCATCGGACCGGACCTTCTCAAAAGACAGATGTGA 1034
Oy 440 LyAlaIaIaThraTyriIleLyAanSerGlnValLeuGlnAARCyAARProGlyAARLeuAan 459
Db 1035 AAAGCGAGCTGGGCTGTCAAACTCTCAAGCGCTC----- 1070
Oy 460 LysTrpTyraGlnhiIleSerLyGlyAlaIaTrpProPheSerThriGlyAanIleGlyTrp 479
Db 1071 -----CTGCGCGGTTGGGCTTTTCACACATCAAAACAAACAT 1109
Oy 480 ProIleSerAARCyThraIaGlnLyLeuLyAlaValLeuLeuSerLyIleAla 499
Db 1110 CCCGATTGAGCATACCGCTGCGGCACTTAAAGCT----- 1145
Oy 500 ProGluIleValGlyGlnProIleAARValLyAARgLeuTyThraSerValAan----- 517
Db 1146 -----ATTCCGTTCAACGCGCTCCGATGATGAGACCGGCGG 1184
Oy 518 -----ValIleLeuSerLeuGlnAanGluAARgLyGlyPheAlaThraTyrgLyLeuLy 535
Db 1185 CTCGCGCTGGCTTTATTCATGCAAAACAGAGCGAGGCTTTGCGGCACTTTGAAGAAAGAT 1244
Oy 536 ArgSerTyraAnTrpLeuGlnIleIleAanProAlaGluThraPheGlyAARlIeValIle 555
Db 1245 GTTACACATCGGCTTATTCGAAATCTG---CCGCTGCAATCTGCGCTGAGGACAGCAGCT 1301
Oy 556 AARTyraProTyraIaGlyCyThraSerAlaAlaIleGlnAlaLeu-----AlaSer 572
Db 1302 GATCCGTCAACGAGCACTTGACCGAGCGGCTTTATCTGCTCGGCGCTTAAAGCGCG 1361
Oy 573 PheArgLyLeuTyTrpGlnLyhiAARgLyGlnLyIleGlnhiCyhiAARLyAla 592
Db 1362 TTCAAGATTAACATCTCTGCGGCTCGGCG-----GCC 1394
Oy 593 ThrThraPheIleGlnLyIleGlnAlaSerAARgLySerTyrgLySerTrpGlyVal 612
Db 1395 CTCAGGTGGCTTATCATCATCAAGAAAGCGAGCGCTCTTGATGCAATGCGGCGCTC 1454
Oy 613 CyAARThraTyrgLyAlaIaTrpPheGlyValLyGlnLyLeuIleAlaIaGlyAARSer 631
Db 1455 TGCATTATTAACGGTATACGGCGCGCACTCACCGGATGTAAGAGCTGTGCGGGTTCC 1511
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RESULT 12
US-09-533-4882
Sequence 4882, Application US/09533559
Patent No. 6902887
GENERAL INFORMATION:
APPLICANT: Randy M. Berka
APPLICANT: Michael W. Rey
APPLICANT: Jeffrey R. Shuster
APPLICANT: Sakari Kaupinen
APPLICANT: Ib Groth Clausen
APPLICANT: Peter Bjørke Olsen
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 5849.200-US
CURRENT APPLICATION NUMBER: US/09/533,559
CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 09/273,623
EARLIER FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4882
LENGTH: 652
TYPE: DNA
ORGANISM: Aspergillus oryzae
US-09-533-559-4882

Alignment Scores:
Pred. No.: 7,72e-25 Length: 652
Score: 302.00 Matches: 76
Percent Similarity: 52.4% Conservative: 35
Best Local Similarity: 35.8% Mismatches: 67
Query Match: 7.3% Indels: 34
DB: Gaps: 8

US-09-419-679-6 (1-757) x US-09-533-559-4882 (1-652)
QY 438 IleaDgLYaIAhIethrYrIleYvaNsersGlnValleuNgIuNarCyPProGIIaAP 457
DB 1 CTCACCAAGCCCTCGAATCTCTGATTAATCACCAACTCGGGAGATGATCA---GAT 57
QY 458 LeuAonLYrTrpYzrgrHsIleSerLYsGlyAlaTrPProPheSerThrGlyAerHIs 477
DB 58 CAGGAGAAATGCTACCTGCTCAGACACCGAAAGGGCGCATGGCCCTTCAGCAACAATACTG 117
QY 478 GIIrTrProIleSerArPCyThraIaGluGlyLeuLYaIaValleuLeuSerLYs 457
DB 118 GGCTATACAGTTAGCAGCATGCACGCGGAGGCTTACGTTCAAGCATTCAGCTTCAAGAG 177
QY 498 Iie-----AlaProGluIleValIGlyuProIleArValYArgrLeuLYzrArPser 515
DB 178 ATGCACAACTATCTTAAACG-----ATATCCACACAGCGCTTAAAGATAGT 225
QY 516 ValaenValIleleuSerleuGlnaenGluArGlyYpheaIaThrYrGluLeuLYs 535
DB 226 GTTGACTGCTGCTGCTCATGCAAAATCTTTCGGCGCTTTTACAGATATGACACACC 285
QY 536 ATGSeTrYAaTrPLeuGluIleleAenProAlaGluThrPheGlyAerIleValIle 555
DB 286 CGTGCGCTCGCCCAAGGTGAGGTGGTGAATGCCGCCGAGGATTTTCGGCGGATTAATGATT 345
QY 556 AArTYrProTYrValIGlyCyThrSerAlaAlaIleGlnAlaSerArPLeuLYs 575
DB 346 GGTTAAGACTATCTGTAAATGACACACAGCTCGCTCATCTGCGCTTTAGTGAGGAGAG 405
QY 576 LeuTYrPro-----GlyNArgrArGluGluIleGlnHIsCyv 588
DB 406 TTCTATTCCTATTACCGATACGACACACATCGGGGGGGCTGACAAACCGTC-----TGT 455
QY 589 IleaArLYaIaThrThrPheIleGluLYaIleGlnAlaSerArPLeuLYs 608
DB 460 GTA-----GCATGACATGCTGTAACGATACGACAGA-----GGG 492
QY 609 SerTrPLeuLYaIleCyPheThrYrGlyAlaTrPProPheLYaIuLYsGlyLeuIleAla 626

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Db 493 CACATGACGCGTGTGTCCTT-----GTACTAGCTGG 525

Qy 629 G1yArSerPheSerAenCySserIleArgIys 640

Db 526 GGAATGGGAACTCCTAAGTGTATGAGATTGGAATA 561

RESULT 13

US-09-725-735A-11

Sequence 11, Application US/09725735A

Patent No. 6645751

GENERAL INFORMATION:

APPLICANT: RUSING, MATTHIAS

APPLICANT: SCHEMELNS, THOMAS

APPLICANT: DRESLER, PETRA

APPLICANT: STOCK, WOLFGANG

APPLICANT: KIV, THOMAS

TITLE OF INVENTION: NOVEL NUCLEIC ACID ISOLATED FROM TETRAHYMENA WHICH

TITLE OF INVENTION: CODES FOR A TETREPHENOID CYCLASE, ITS PRODUCTION AND

TITLE OF INVENTION: USE

FILE REFERENCE: 25426.0001

CURRENT APPLICATION NUMBER: US/09/725.735A

CURRENT FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: DE 199 57 889.3

PRIOR FILING DATE: 1999-12-01

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 11

LENGTH: 2072

TYPE: DNA

ORGANISM: Tetrahymena thermophila

US-09-725-735A-11

Alignment Scores:

Pred. No.: 6.11e-12 Length: 2072

Score: 198.00 Matches: 160

Percent Similarity: 35.2% Conservative: 96

Best Local Similarity: 22.0% Mismatches: 247

Query Match: 4.8% Indels: 226

DB: 3 Gaps: 41

US-09-419-679-6 (1-757) x US-09-725-735A-11 (1-2072)

Qy 108 G1nCvSH1aerG1yH1aItr-----ProG1yAerTyG1yIyProMetPheIeu---- 124

Db 145 GAAAGTACACAAACAAATAGTGTACTATCT--CCTTACTTAAGCGAAATGTTATGACT 201

Qy 125 -----MetProG1yLeuValIleThrLeuSerIleThrG1yAlaLeuSnn--Thr 140

Db 202 GAATCTACTTGGAGTACTCTGCTTTGAATTGGACATTAATCTGCTTTCAACGGCTACA 261

Qy 141 ValIeuThrG1uG1uH1aerG1ySg1uIleCySArG1yIleuTyraSnnH1sg1nAnIlyS 160

Db 262 TACTTTACAGAACTG-----CTCCTTAAGACTTAATTCGAA 297

Qy 161 AarG1yG1yTrp---G1yLeuH1aIleG1uG1yProSerThr-----MetPheG1ySer 177

Db 298 GATGGTTCATGGAGCACTGACAGAAACAAATCTTGAACCTGGTTAGTATGCTACT 357

Qy 178 ValIeuSerTyIleThrLeuArgLeuSg1yG1uG1yProSnnAerG1yG1nG1yG1u 197

Db 358 GTCTTTACTACTGATGCTTAAGTGTATTAACAACATCCATAAATT---GAAGCTGCT 414

Qy 198 MetG1uLyAlaArgAarTrpIleleuG1yH1aerG1yAlaIleThrTyTleThrSerTrp 217

Db 415 CATATAAAGGCTAAGAAATGATGATGCTTGAAGGCTGATTAAGCACTCAACATG 474

Qy 218 G1yLeuMetTrpLeuSerValIeuG1yValTyG1uTrpSerG1yAenSnnProIeuPro 237

Db 475 ACCAAATTTAAGTATGACGCTTCGGTTAATACAGTTGGGA----- 516

Qy 238 ProG1uIleTrpIeuLeuProTyMetIeuProPheH1aerProG1yArG1yMetTrpCySnnH 257

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Db      517 ---GATTATGATATGCCATTGTCATC---TTCAAGTAGAATGAAATTTTC----- 564
Qy      258 CysArgMetValTyrLeuProMetSerTyrLeuTyrGlyValArgPheValGly----- 275
Db      565 -----AAATATACCTACGTTAAGATATTTGTCATATAG 600
Qy      276 -----ProIleSerProThrValLeuSerLeuArg-----LysGluLeuTyrThrVal 291
Db      601 GCTATCCACATTTAAGCTGCTTACTTATTTGGCTTACTAAGAAACGTTTTCATGTT 660
Qy      292 ProTyrHisAspIleAspTTrpAspIleAlaArgAsnLeuCyValAlaGlyLeuAspLeuTyr 311
Db      661 CCTGTTGCTGATTTG-----AGAGAG----- 681
Qy      312 TyrProHisProLeuValGlnAspIleLeuTTrpAlaSerLeuHisLeuPheLeuGlnPro 331
Db      682 -----CTCTGG----- 687
Qy      332 IleLeuMetHisTrpProGlyLysArgLeuArgGlyValAlaIleIleSerAlaLeuGlu 351
Db      688 -----ATCAATTAACCTTAAGAACGGTATTAA-----ATCAGTCCCAAGAGAA 729
Qy      352 HisIleHisTyrGlnAspGlnAsnThrArgTyrIleCysIleGlyProValAsnLysVal 371
Db      730 -----TACTCTACACTTAATCCGTATAGCATCTC 759
Qy      372 LeuAsnMetLeuCysCysTyrValGlnAspProAsnSerGluAlaPheLysLeu----- 389
Db      760 TTGATCTTAATG-----GACGAAATCTTCAAACTTAACAA 795
Qy      389 ----- 389
Db      796 CCTCTGGAAGTTTGGTGCCTACACTATTTCACCCCTTGACTTAAATGCTTCAA 855
Qy      390 -----HisLeuProArgIleTyr-----AspTyrLeuTTrpIleAlaGlu 402
Db      856 GACTTTTAGTCAAAACAC---CCTCATCTATACAAAAGAAATCAAAAGGCTTACCAA 912
Qy      403 AspGlyMetLysMet-----GlnGlyTyrAsnGlySer 413
Db      913 GACGGATACTATTCTGAGTTTAACATCTTAACTTTAAGAGAACTTATACACGGCTCT 972
Qy      414 -----GlnLeuTTrpAspThrAlaPheAlaValGlnAlaIleIleAlaSerAsn 429
Db      973 TTGGATGATGGTAGATGGTGGATAC-----ATTCTTATTAAGTTGG 1014
Qy      430 LeuIleGluGlnPheGlyProThrIleArgLysAlaHisThrTyrIleLysAsnSerGln 449
Db      1015 GCTATGCTTGAAGTGGCTAAGATTAAGAAAGAAATCTTCCCTATGCTATAAATATG--- 1071
Qy      450 ValLeuGlnAspCysProGlyAspLeuAsnLysTyrTyrArgHisIleSerLysGlyAla 469
Db      1072 -----GTCAAGAAAGCTTT 1086
Qy      470 TrpProPheSerThrGlyAspHisGlyTyr-----ProIleSerAspCys 484
Db      1087 TAACCTAAAAAAGATAGATTATGATATGATTTGCAATATGCTCCGACACATATAC 1146
Qy      485 ThrAlaGlnGlyLeuLysAlaValLeuLeu-----LeuSerLysIle 498
Db      1147 ACT-----GGATTACTTCTGCTGTATGAGTACTACAAAGAACCTTCAAAAGTAA 1200
Qy      499 AlaProGlnIleValGlyGlnProIleAspValLysArgLeuTyrAspSerValAsnVal 518
Db      1201 ATCCCTGAA-----ACTATGAAATGG 1221
Qy      519 IleLeuSerLeuGlnAsnGlnAspGlyGlyPheAlaThrTyrGlu----- 533
Db      1222 CTTTCTCTATGCAAAATGACATGATGCTTCTTTCAGCTTTGACAAAGGATAAAAATGAA 1281
Qy      534 -----LeuLysArgSerTyrAsnTTrpLeuGlnIleIleAsnProAlaGlnThr 549
Db      1282 GACAATTTATTTGTTCAAGTTTGCCTTCAATATAGGTGATTTGCTTAACGCTGAATC 1341

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Qy      550 PheGlyAspIleValIleAspTyrProTyrValGlnCysThrSerAlaAlaIleGlnAla 569
Db      1342 TTC-----GATCCCTCATGTCCTGATATTACTGTCATCATATGGAAGGA 1386
Qy      570 LeuAlaSerPheArgLysLeuTyrProGlyHisArgArgGlnGlnIleGlnHisCys-- 588
Db      1387 TTGGGTGAGTTT-----GGATAT-----CAAGCTAATCATCTTTAG 1422
Qy      589 IleAspLysAlaThrThrPheIleGlnLysIleGlnAlaSerAspGlySerTTrpTyrGly 608
Db      1423 ATTTAAATATGATTAAATATCAAGAAAGCTTGAACAAGTGGGATTTGGTTAAGCT 1482
Qy      609 SerTTrpGlyValCysPheThrTyrGlyAlaTrp-PheGlyValLysGlyLeuIleAlaI 628
Db      1483 AGATGGGGTGTAAATTATCAT-TATGCTGTTGGAGCTGTTTACACAGTTTACGAAGAGT 1541
Qy      628 aglyArgSerPheSerPheSerSerIleArgLysAlaCysGlnPheLeuLeuSerLys 648
Db      1542 CAATTACGACTTA---AATGAACAGTGGGTACAAATAGATTAATTAATTGCTTAATTA 1598
Qy      648 aglnLeuProSerGlyGlyTTrpGlyLysSerTyrLeuSerCysGlnAsnLysValTyrSe 668
Db      1599 ATTAATTAAGATGTGGCTTTGGTGAATGTCTTCTTATATATGATCTGAAAGGTG 1658
Qy      668 rAsnLeuGlnGlyAsnArgSerHisValIleAsnThrGlyTTrpAlaMetLeuAlaLeuI 688
Db      1659 GAATGCTATAGT---AAATTAAGTCTACCTCAAACTCATGGGAGCTATTAAGCTCTTTT 1715
Qy      688 eAspAla-----GlyGlnAlaLysArgAspSerGlnProLeuHisArgAlaAl 704
Db      1716 AGAGTTTATATTAATTAATTAATGAACAAATTAAGCATGTCGACAT-----AGAGCTGC 1766
Qy      704 alaTyrLeuIleAsn---SerGlnLeuGlnAspGlyAspPheProGlnGlnIleLeu 723
Db      1767 TTAGTATTTTATTAATTAATTCAAAGAGATTAATACCTTATATGATCATCTCACAT 1826
Qy      723 tGlyValPheAsnLysAsnCysMet---IleThrTyrAlaAlaTyrArgAsnIlePhePr 742
Db      1827 AGGAACAGCTCACAGAGATTAATCTTATTTATAGTACCCTCATATGCAATCATTTCC 1886
Qy      742 oIleTTrpAlaLeuGlyGlyTyr 749
Db      1887 ATTAGTAGCTTAAATAGATAC 1908

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RESULT 14
 US-10-104-047-1011
 ; Sequence 1011, Application US/10104047
 ; Patent No. 6943241
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: NO. 6943241el full length cDNA
 ; FILE REFERENCE: H1-A0105
 ; CURRENT APPLICATION NUMBER: US/10/104,047
 ; PRIOR FILING DATE: 2002-03-25
 ; NUMBER OF SEQ ID NOS: 4096
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1011
 ; LENGTH: 3600
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-104-047-1011

Alignment Scores:
 Pred. No.: 4,11e-08 Length: 3600
 Score: 168.50 Matches: 32
 Percent Similarity: 67.7% Conservative: 10
 Best Local Similarity: 51.6% Mismatches: 19
 Query Match: 4.1% Indels: 1
 DB: 3 Gaps: 1

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1	124.8	4.9	1440	7	US-11-217-529-5566	Sequence 5566, App
2	120.6	4.7	642	7	US-11-217-529-5565	Sequence 5565, App
3	116.4	4.5	696	7	US-11-217-529-173919	Sequence 173919, App
4	172.6	2.8	750	7	US-11-217-529-174234	Sequence 174234, App
5	43.2	1.7	516	7	US-11-217-529-166803	Sequence 166803, App
6	36.2	1.4	972	6	US-10-136-749-443	Sequence 443, App
7	36	1.4	478	6	US-10-473-173-292	Sequence 292, App
8	36	1.4	478	6	US-10-488-619-82	Sequence 62, App
9	36	1.4	822	6	US-10-505-928-811	Sequence 822, App
10	36	1.4	1689	7	US-11-217-529-1941	Sequence 1941, App
11	35.6	1.4	377	6	US-10-488-619-1909	Sequence 1909, App
12	34.2	1.3	835	6	US-10-488-619-2360	Sequence 2360, App
13	34.2	1.3	1722	6	US-10-505-928-554	Sequence 554, App
14	34	1.3	70665	6	US-10-505-928-596	Sequence 596, App
15	33.8	1.3	1692	7	US-11-217-529-551	Sequence 551, App
16	33.4	1.3	1410	7	US-11-217-529-82049	Sequence 82049, App
17	32.8	1.3	757	6	US-10-488-619-2096	Sequence 2096, App
18	32.8	1.3	852	7	US-11-217-529-77022	Sequence 77022, App
19	32.8	1.3	1256	6	US-10-505-928-671	Sequence 671, App
20	32.8	1.3	1582	7	US-11-222-810-10	Sequence 10, App
21	32.8	1.3	1582	7	US-11-222-810-12	Sequence 12, App
22	32.8	1.3	3441	7	US-11-217-529-19924	Sequence 79924, App
23	32.6	1.3	1830	7	US-11-217-529-1897	Sequence 1897, App
24	32.6	1.3	2414	6	US-10-511-937-389	Sequence 389, App

100

Db 652 TGGCTACTTCGGTACTCATTTGCCATTTCATCCAGGAGATGGTGGTTCATACTAGAGCC 711

Oy	805	GTCTATTTTCCGATGTCCTACTTATATGCGAAGAGTTGTGTGCCATCTCACCACA	864
Db	712	GTTTACATTTCCAGTAGTTACCTGTCATTTGGTAAAGTTGTATGTCCTCAGTACTCTT	771
Oy	865	GTATATCTTTGAGAAAGAGCTTATACAGTACCATACCATGATATATGATGGGATCG	924
Db	772	CTTGAAAGATTGAGGGGTGAATTTTACGTCAAAACCTTTGATAGATTACCTTTCTAAC	831
Oy	925	GCTGCAATTTGTGTGCAAAAGGAAATTTGTACTATCTCACCACACTTGACAGATAT	984
Db	832	CACAGAAACACTGTGTGTGAGGTGATTTATATATCCACACTTAAATTTTGAATAT	891
Oy	985	CTTTGGGCACTCTACACAGTTCTTGAGCTTATCTGATSCATTTGGCTGGAAAAAGA	1044
Db	892	GCAATTTGTTTGTGTATTTTACGAAAAATCTTGAGAAATCGATTCTATTTCTCTTA	951
Oy	1045	TTGAGGAAAAAGGCTATATTTCTGCATTTGAGCATATACATTAAGAAATGAGATCT	1104
Db	952	TTCCAGAGAAAAAGTT-----TACGACCTGATTTAAAAAGAAATTTAAAAATCC	999
Oy	1105	CGATATATTTGCATAGAGTCTGTATATATAGAGTTAAATATGCTTGCTGTGGGTGAA	1166
Db	1000	GATTTCTTTGTGTATGACCTGTATATCAAGATTTTGTGCCCTTGTACTTAAATGGA	1055
Oy	1165	GATC---CAAAATTCGAGGCTTCAAGTTGCATCTTCCACGAGTTTATGATATCTATG	1221
Db	1060	GATGTTGATGANTCAAAAGCCTTCAAAAGTTCCAAATACAGTTCAAGATTCATTTGTT	1111
Oy	1222	ATTGCAGAAATGCGATGAAAAATGCAAGGCTACAAATGGAATGCACTATGSGACCTGT	1281
Db	1120	CATGGCCCAAGGGCATGACCTTTATGGAACCAACGGGTGTCAAACTTGGGACGTGCA	1175
Oy	1282	TTTGCTGTCCAAAGCAATATTCATCTTACCTCATTTGAAGATTTGTGCCACTATTAAG	1341
Db	1180	TTTGCAATTCATATATTTTTTTTACTGTGTGTGCGAGAAAGCCGAAATTTTATTAACA	1233
Oy	1342	AAAGCTCACTTATATTAAGAATTCACAGGTTTATAGAAGTTGCCAGTATCTTAT	1401
Db	1240	ATTGCTCCGCTATTAATTTCTGTGTGTTCTCAGTTTGACACTGAATGCGTTCTGT	1291
Oy	1402	AAATGTTACCGTCACATTTCAAAAGGTCTTGGCCTTTTTCACATGAGATCATGATGG	1461
Db	1300	A---GTTTAAAGACAAAAGAAAGAGTGTGGGGTTTTTCAACAAAGACTCAAGTTAT	1355
Oy	1462	CCAAATTTTGTACTGCACGCTGAAGAGACTGAAAGCTGTTCTATTACTA	1509
Db	1357	ACGGTTTCTGACTGTACAGAAATGATTCACAGGCTATATATCATGTA	1404

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RESULT 2
US-11-217-529-5565
? Sequence 5565, Application US/11217529
? Publication No. US2006009612A1
? GENERAL INFORMATION:
? APPLICANT: SUNTORY LIMITED
? APPLICANT: NAKAO, YOSHIHIRO
? APPLICANT: NAKAMURA, NORIHISA
? APPLICANT: KODAMA, YUKIKO
? APPLICANT: FUJIMURA, TOMOKO
? APPLICANT: ASHIKARI, TOSHIHIKO
? TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
? FILE REFERENCE: S-38-285
? CURRENT APPLICATION NUMBER: US/11/217,529
? CURRENT FILING DATE: 2005-09-02
? PRIOR APPLICATION NUMBER: US 10/932,182
? PRIOR FILING DATE: 2004-09-02
? NUMBER OF SEQ ID NOS: 197023
? SOFTWARE: PatentIn version 3.3
? SEQ ID NO 5565
? LENGTH: 642
? TYPE: DNA
? ORGANISM: Saccharomyces pastorianus

```

US-11-217-529-5565

Query Match	4.7%	Score 120.6;	DB 7;	Length 642;
Best Local Similarity	53.3%;	Pred. No. 4.7e-24;		
Matches 330; Conservative	0;	Mismatches 274;	Indels 15;	Gaps 3;

OY	1646	TGGAGATTAATCAATCTCGTGAAACTTTTGGTGCATCGTAATTGATTATCTTATGTCG	1705
Db	2	TGGAGAACTTAATCTCACTGAAGTTTTTCGGTAACATCATGTGAATATCCCATACGTGG	61
OY	1706	AATGTACATCAGCAGCATTCAGCTTTGGCATCATTTAGAAATTAATATCTGGGCATC	1765
Db	62	AGTGACACAGATCTTCGCTTCCTGGACTGACCTCTTCATTAAGTTTT---TGACTATA	118
OY	1766	GCCGAGAAAGAAATCAACATTTGATTCGATTAAGCACTACCTTGATGAAAAAATACAAAG	1825
Db	119	AAAAAGGAAATATCTACATGATATCAGAAATCGCTATTGAAATACATCAAGAACTCAAC	178
OY	1826	CTTCAGATGATCATGTGATATGTTCTTGGGAGTTTGTCTCACTACGSGCTGGTTTG	1885
Db	179	TACACAGAGGAGGTGGTATGGAAGCTGGGGTATTTGCTTCACTATCAGATATGTTTG	238
OY	1886	GGGTAAAAAGTCTGATTCCTGCTGGAAGAGTTTCAGTAATTCGTCAAGCATCCGTAAAG	1945
Db	239	CGTTGAAAGCATCAACACTGTGGAGAAATATCGAAATTTCTTCGACGGTGAAGAAAG	298
OY	1946	CTTGTGATTTCTGCTGTCCAGAGAGCTTCCTTGTGTGCTGGGAGAGAGTTATCTGT	2005
Db	299	GTTGTGATTTCTGTGTAGCAAGCAGATGAAGACGGTGGTGGGGTAAATCATGATGAAGT	358
OY	2006	CTGTCAAAACAAAGTGTATTCAAATCTGGAAGCAACAGTCTCATGTGTTCAACTG	2055
Db	359	CTAGT-----GAATGTGATATGTTATGTGATATGAAGACTCTGTAGTCTCCAAAG	412
OY	2066	GATGGGCTATGTTGCTCTCATTTGATGCTGGACAGGCTAAGAGAGATTCGCAACCATCGC	2125
Db	413	CATGGGCACTGATTGCACTGCTTTTGTCTGAATCCGAAAGAAAGS-----TCAITG	466
OY	2126	ACCGGCGACTGCATCTTGATTAATTCCTCAATTGGAAGACGGTGAATCTTTCGACGACGG	2185
Db	467	ACCGAGGTATTGAGCTTTTAAAGCATGACACAAAGAAATCCGAGAAATGAAATTTTGGA	526
OY	2186	AAATATATGGAGTCTTCAAACAAGATTCATGATCATATCGCGCATACAGAAACATAT	2245
Db	527	GCGTGAAGAGTGTTTTAATCATTCCTGTGCAATCGAATACCCAAAGTTATAGATTTTGT	586
OY	2246	TCCCCAATTGGCGTTGGG 2264	
Db	587	TTCCCATAAAGCAATTAGG 605	

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RESULT 3
US-11-217-529-173919
Sequence 173919, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHITIRO
APPLICANT: NAKAMURA, NORIHIISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIIKO
TITLE OR INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 173919
LENGTH: 696
TYPE: DNA

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ORGANISM: Saccharomyces pastorianus
US-11-217-529-173919

Query Match 4.5%; Score 116.4; DB 7; Length 696;
Best Local Similarity 54.5%; Pred. No. 6.9e-23;
Matches 281; Conservative 0; Mismatches 226; Indels 9; Gaps 2;

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QY 1596 TGAAGATGGTGGTTTGCACATATGAGCTTAAACGATCTTAAATGGTTGAGATAT 1655
DB 108 TGAATATGGTTCCTTTGCACATATGATTAATCAAGGCCCATGACATGAAACCTT 167
QY 1656 CAATCTGTGTAACCTTTGGGACATGCTTATGATTAATCTTATGCGAATGTAATC 1715
DB 168 GAATCTGTGTAAGTTTGGGACATATGATTAATGTAATGTAATGTAATGTAATGTA 227
QY 1716 AGCAGCATATGAGCTTGGGACATATGATTAATGTAATGTAATGTAATGTAATGTA 1775
DB 228 TTCAATCCGTTCTGGGGTTCATATTTTCAAA---GTACTTCGACTATGAAAGAGA 284
QY 1776 AATACAACTTGTATGATTAAGCACTACCTTCAATGAAATAATCAAGCTTCAGATG 1835
DB 285 AATACGTAACAGCATAGAAATGCCATCGAATTCATTAATAAATCTCAATTAACGATG 344
QY 1836 ATCATGTAATGCTTCTGGGAGTTGCTTCACTTAACGCTGCTGTTGGGGTAAAG 1895
DB 345 AAGTGTATGGAAGCTGGGGTATTTGTTTACATATGCGGTATGTTGCAATGAGGC 404
QY 1896 TGTGATGTGCTGGGAAGGATTTGATTAATGCTCAACATCCGTAAGCTTGTGAT 1955
DB 405 AATACACACCGTGGGGAGACCTATGAGAAATTCCTCAACGTAAGAAAGTTGCGACT 464
QY 1956 TCTGCTGTCAAGCAAGCTTCTTCTGTGTGCTGGGAGAGATTAATCTGCTCAAA 2015
DB 465 CTGTGCTAGTAACAGATGAAGATGGCGTTGGGGGATCAATGAATGCCAGTAAAT- 523
QY 2016 CAAGGTATTAATCAATCTGGAAGCAACAGCTCTCATGTGTCACACTGGTGGCTAT 2075
DB 524 -----TACATGATTAATGATGATGTAAGAAATCGCTAGTGTTCAAACCGACGCGCT 578
QY 2076 GTTGGCTCATGATGCTGGAAGGCTAAGAGA 2111
DB 579 AATGCACTTCTTTGCTGAAATATCTTAATTAAGA 614

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RESULT 4
US-11-217-529-174234

Sequence 174234, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIRO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
PRIOR FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 174234
LENGTH: 750
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-174234

Query Match 2.8%; Score 72.6; DB 7; Length 750;
Best Local Similarity 53.8%; Pred. No. 6.9e-11;
Matches 175; Conservative 0; Mismatches 144; Indels 6; Gaps 1;

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QY 505 GATGCTGGGAGGGGTTTGCATATTAAGATCCAGACCATGTTTGGCTGTCTTGAAT 564
DB 418 GATGCTGGGAGGGGTTTGCATATTAAGATCCAGACCATGTTTGGCTGTCTTGAAT 477
QY 565 TATATTAATCTAGATTTGCTAGTGAAGGGGCTTAATGAGCAAGGGGAAATGAGAG 624
DB 478 TATGTAATCTTAAGTTTATTT-----GGGTCTACCAAGACACCCGGTTTGGCCCAAG 531
QY 625 GCACGTGATGATTTCTAGGCGATGTTGCTGCTACTTATATTAAGCTATGAGGGAAGATG 684
DB 532 GCAAGAAACCAATGTTTAAAGTTAGGCGGTCTATTTGATCCCTCACTGGGGGAAATTT 591
QY 685 TGGCTTTAGTACTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 744
DB 592 TGGCTTAAGTGACTTAACCTTGTATTAATGGAAGGTGGAACCTTGGCTTCTGAAACT 651
QY 745 TGGCTCTTCAATACATCTTCAATTTCTCAATTCAGAGAGATGTTGTTCACTGCCGATG 804
DB 652 TGGTTACTTCCATATTCATGCTGCCATGATCCGGGAGATGTTGGGTTTCACTAGAGAT 711
QY 805 GTCTATTTGCGAGTGTCTTACTTAT 829
DB 712 GTTATCATTTCCGTTCACTTACTGT 736

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RESULT 5

US-11-217-529-166803
Sequence 166803, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIRO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
PRIOR FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 166803
LENGTH: 516
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-166803

Query Match 1.7%; Score 43.2; DB 7; Length 516;
Best Local Similarity 50.4%; Pred. No. 0.0063;
Matches 133; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

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QY 1097 AGAATATCTGATATATTTGCATAGGCTCTGTAAATAGGTGTTAAATATGCTTGTGTT 1156
DB 233 AGAATATCTGATATTTGCTATATAGCACTGTAAACCAAGCGTTTGGCGACTGTACTC 292
QY 1157 GGGTGAAGA---TCCAATTTGAGGCTTCAAGTTGATCTTCCAGATTTATGATT 1213
DB 293 TTATTTGAAGAGGGGTGAGCTGGAAGCTTTCAGAGGTTTCCAATATAGATTCAAGATG 352
QY 1214 ATCTATGATTCAGAAAGATGCAATGAATGCAAGGCTTAATGGAATGCAATGATGAG 1273
DB 353 CATTTTCAATGTTGCAAGAGGATGACCATATATGGAACAATATGTTGCAAACTGGG 412
QY 1274 ACACTGCTTTTGTGTCAGCAAGCAATTTATGCACTTAACCTCATGAAATTTGTCGA 1333
DB 413 ATTTGCGTTTGTGCAATTAATCTTTTGTGTGCGAGGCTTCGAGAAAGACCTGAATTC 472
QY 1334 CTATAGAAAGGCTCACTTATA 1357
DB 473 ATTAACAATTTGCTGCTTATA 496

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RESULT 6
US-10-196-749-443
; Sequence 443, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 443
; LENGTH: 972
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-443

Query Match      1.4%; Score 36.2; DB 6; Length 972;
Best Local Similarity 59.0%; Pred. No. 0.72;
Matches 62; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Cy      2456 AGAATGCGTGAAGTTTTCATATACATGAGCGCTCTGCTTCCCTGAGAG 2515
Db      853 AGAGTCTGTAGAGTCTCTAATTAATATGTCCTCTATTCCTCAACAATTA 912

Cy      2516 AGGAATTAATATATACATTAATAGAGATATATATATATATATATATAT 2560
Db      913 AGGATTTTGCATATGAAAAAATATATATATATATATATATATATATATAT 957

RESULT 7
US-10-473-173-292
; Sequence 292, Application US/10473173
; Publication No. US2006008823A1
; GENERAL INFORMATION:
; APPLICANT: VAN ANDEL INSTITUTE
; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
; TITLE OF INVENTION: Carcinoma: Prognosis and Drug Target Identification
; FILE REFERENCE: 38345-170094
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; CURRENT APPLICATION NUMBER: US/10/473,173
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/279,411
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 498
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 292
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (409)..(409)
; OTHER INFORMATION: n can be a, c, g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (427)..(427)
; OTHER INFORMATION: n can be a, c, g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n can be a, c, g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (452)..(452)
; OTHER INFORMATION: n can be a, c, g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (458)..(458)
; OTHER INFORMATION: n can be a, c, g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (467)..(467)
; OTHER INFORMATION: n can be a, c, g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (472)..(472)
; OTHER INFORMATION: n can be a, c, g or t
US-10-473-173-292

Query Match      1.4%; Score 36; DB 6; Length 478;
Best Local Similarity 56.9%; Pred. No. 0.57;
Matches 66; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Cy      1418 TTTCAAAGGTCGTGGCTTTTTCATGAGATCATGATGCGCAATTTGACGTGCA 1477
Db      186 TTCAGAAAGTCTTGAGCTGTAATAGAGATGCAATTTGACGTGTT 245

Cy      1478 CAGCTGAAGAGCTGAAGCTGTTCTATTAATCTCAAAATTTGACCAAGAAATAGTT 1533
Db      246 TCTGTGCCAACAAGAAAGTTTCACAAATGCTTTCCAAACTGCATATAAAGAACTT 301

RESULT 8
US-10-488-619-62
; Sequence 62, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(478)
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OTHER INFORMATION: n 1s g, c, a o r t
US-10-488-619-62

Query Match 1.4%; Score 36; DB 6; Length 478;
Best Local Similarity 56.9%; Pred. No. 0.57;
Matches 66; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1418 TTTCAGAAAGTCTGGCCCTTTTCAACTGAGATCATGATGCCAATTCTGACTGCA 1477
DB 186 TTTCAGAAAGTCTGTAGCTGTAAATGAGAAATATGATGTAATTTGACTGTT 245
QY 1478 CAGCTGAGAGACTGAAAGCTGTCTATTCTATCCAAATTCACAGAAATAGTT 1533
DB 246 TCTGTGCCAAGACAGAAAGTTTCAAAATGCTTCCAACTGCATTAAGAAACTT 301

RESULT 9
US-10-505-928-411/c

Sequence 411, Application US/10505928
Publication No. US20060088532A1

GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et al.

TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

FILE REFERENCE: 28967/39178

CURRENT APPLICATION NUMBER: US/10/505,928

PRIOR FILING DATE: 2004-08-27

PRIOR APPLICATION NUMBER: US 60/363,019

NUMBER OF SEQ ID NOS: 866

SOFTWARE: PatentIn 3.2

SEQ ID NO 411

LENGTH: 822

TYPE: DNA

ORGANISM: Homo sapiens

US-10-505-928-411

Query Match 1.4%; Score 36; DB 6; Length 822;
Best Local Similarity 56.9%; Pred. No. 0.75;
Matches 66; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1418 TTTCAGAAAGTCTGGCCCTTTTCAACTGAGATCATGATGCCAATTCTGACTGCA 1477
DB 635 TTTCAGAAAGTCTGTAGCTGTAAATGAGAAATATGATGTAATTTGACTGTT 576
QY 1478 CAGCTGAGAGACTGAAAGCTGTCTATTCTATCCAAATTCACAGAAATAGTT 1533
DB 575 TCTGTGCCAAGACAGAAAGTTTCAAAATGCTTCCAACTGCATTAAGAAACTT 520

RESULT 10
US-11-217-529-4941

Sequence 4941, Application US/11217529
Publication No. US20060099612A1

GENERAL INFORMATION:

APPLICANT: SUNTORY LIMITED

APPLICANT: NAKAO, YOSHIHIRO

APPLICANT: NAKAMURA, NORIHISA

APPLICANT: KODAMA, YUKIKO

APPLICANT: FUJIMURA, TOMOKO

APPLICANT: ASHIKARI, TOSHIHIRO

TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

FILE REFERENCE: S-38-285

CURRENT APPLICATION NUMBER: US/11/217,529

PRIOR FILING DATE: 2005-09-02

PRIOR APPLICATION NUMBER: US 10/932,182

NUMBER OF SEQ ID NOS: 197023

SOFTWARE: PatentIn version 3.3

SEQ ID NO 4941

LENGTH: 1689

TYPE: DNA

ORGANISM: Saccharomyces pastorianus

US-11-217-529-4941

Query Match 1.4%; Score 36; DB 7; Length 1689;
Best Local Similarity 51.2%; Pred. No. 1.1;
Matches 84; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 1310 ACCCTATGAGAAATTTGCTCAACTATTAAGAAAGCTCATACCTATTAAGAAATTCAC 1369
DB 1490 ACAAAATCTTACCACTCCGGCGCACTATTGGAACAAGAAACCTTAATGAATATGAAC 1549
QY 1370 AGGTTTGAAGATTGTCCAGGTGATCTTAATTAATGATCCGTCACATTTCAAAAGTG 1429
DB 1550 CGTTTACGATTAATCTATATGATATGAACGAAGAGTGACGATCAGCATTAAGATCCG 1609
QY 1430 CTGGCCCTTTTCAACTGAGATCATGATGCCCAATTTTCAC 1473
DB 1610 AAGGACTTTTATGATTAATGATGATTAACGAAGAGATGATCATGAC 1653

RESULT 11
US-10-488-619-1909

Sequence 1909, Application US/10488619
Publication No. US20060099578A1

GENERAL INFORMATION:

APPLICANT: Greenlee, Warner and Sullivan, P.C.

TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations

FILE REFERENCE: 98-01 WO

CURRENT APPLICATION NUMBER: US/10/488,619

PRIOR FILING DATE: 2004-03-01

NUMBER OF SEQ ID NOS: 3040

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1909

LENGTH: 377

TYPE: DNA

ORGANISM: Mus musculus

US-10-488-619-1909

Query Match 1.4%; Score 35.6; DB 6; Length 377;
Best Local Similarity 67.6%; Pred. No. 0.65;
Matches 50; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1332 AACTATTAAGAAAGCTCACTATTAATTAAGAAATTCACAGGTTTGAAGATGTCACAG 1391
DB 2 AATTTTAAAGAGCGCATCAATTTATTAAGAAATTTGAAGTTTAAAAATGATTAAG 61
QY 1392 TGATCTTAATAAT 1405
DB 62 GAGATTTATTAAT 75

RESULT 12
US-10-505-928-842/c

Sequence 842, Application US/10505928
Publication No. US20060088532A1

GENERAL INFORMATION:

APPLICANT: Ludwig Institute for Cancer Research et al.

TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

FILE REFERENCE: 28967/39178

CURRENT APPLICATION NUMBER: US/10/505,928

PRIOR FILING DATE: 2004-08-27

PRIOR APPLICATION NUMBER: US 60/363,019

NUMBER OF SEQ ID NOS: 866

SOFTWARE: PatentIn 3.2

SEQ ID NO 842

LENGTH: 7280

TYPE: DNA

ORGANISM: Homo sapiens

US-10-505-928-842

Query Match 1.4%; Score 34.6; DB 6; Length 7280;
Best Local Similarity 50.9%; Pred. No. 5.4;
Matches 82; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy	Db	Qy	Db	Qy	Db
2326	ATTATTTGCACCTGTGACAGATAAAGAAATATATATATACCTATTTTTCTTTATTT	2385	7018	AGTCATTTGAAGTGGGCACTACTAACATATTTTATTTTAAAAAATCTTGGCTGTTCTTT	6959
2386	CCATGGCTCTCTTAAATAGTTTGGACATAATGAGTTTAGTCAAGCTTAAAAAAGC	2445	6958	GCCGTGTTCTTTCAAAGAAATTTTAAATATGACTTTAGCTTTTAAAAAATACATAAGG	6899
2446	AAACACGTGAGAAATGCCTGTAAAGTTTTTCTATTAACAT	2486	6898	AAATATATACATCTTATATATAGAAACATTTTACACGTAT	6858

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RESULT 13
US-10-488-619-2360
! Sequence 2360, Application US/10488619
! Publication NO. US2006009578A1
! GENERAL INFORMATION:
! APPLICANT: Greentree, winner and Sullivan, P.C.
! TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
! TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
! FILE REFERENCE: 98-01 WO
! CURRENT APPLICATION NUMBER: US/10/488, 619
! CURRENT FILING DATE: 2004-03-01
! NUMBER OF SEQ ID NOS: 3040
! SOFTWARE: PatentIn version 3.1
! SEQ ID NO 2360
! LENGTH: 835
! TYPE: DNA
! ORGANISM: Mus musculus
US-10-488-619-2360

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Query Match	1.3%	Score 34.2;	DB 6;	Length 835;
Best Local Similarity	67.6%	Pred: No. 2.3;		
Matches 48; Conservative	0;	Mismatches 23;	Indels 0;	Gaps 0;

QY	1333	TATTAAGAAAAAGCTCATACCATATATTAGATTTCACAGCTTTAGAAGATTGTCAGGTGA	13394
Db	28	TTTTTAAAAAAGCGCATACATTTATTATTAAGAATTGGAATTAAATAATGATTAAAGGGGA	87

QY	1395	TCTTAATAAAT	1405
Db	88	GTAATTATAAAT	98

RESULT 14
US-10-505-928-254
; Sequence 254, Application US/10505928
; Publication No. US20060088532A1

```

1  APPLICANT: Ludwig Institute for Cancer Research et al
2  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
3  TITLE REFERENCE: 28967/39178
4  CURRENT APPLICATION NUMBER: US/10/505,928
5  CURRENT FILING DATE: 2004-08-27
6  PRIOR APPLICATION NUMBER: US 60/363,019
7  PRIOR FILING DATE: 2002-03-07
8  NUMBER OF SEQ ID NOS: 866
9  SOFTWARE: PatentIn 3.2
10 SEQ ID NO 254
11 LENGTH: 1722
12 TYPE: DNA
13 ORGANISM: Homo sapiens
14 US-10-505-928-254

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Query Match	1.3%	Score 34;	DB 6;	Length 1722;
Best Local Similarity	57.5%;	Pred. No. 3.8;		
Matches	61;	Conservative	0;	Mismatches 45;
				Indels 0;
				Gaps 0;

Qy 2454 GGAGAAATGCTGTAAAGTTTTCATTAATCTATAGAGCGCTCTCTGTGCTTTCCTGCAGC 2513

Db 1617 GGAGAAATTCCTGTAAATTTCTTAAGTTTGTATTTAAACAATTATGCCACTCGATGCAC 1676

QY	2514	AGAGGAATTAAATATATACATAAATAGAGATATAAAAAAAAA	2559
Db	1677	AAACATATATAATACATAAAGATTAAAAAAAAAAAAAAAAA	1722

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RESULT 15
US-10-505-928--596/c
; Sequence 596, Application US/10505928
; Publication No. US20050089532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 596
; LENGTH: 70665
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928--596

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Query Match	1.3%	Score 33.8;	DB 6;	Length 70665;
Best Local Similarity	53.4%	Pred. No. 28;		
Matches 71;	Conservative 0;	Mismatches 62;	Indels 0;	Gaps 0;

QY	2415	ATAGATTGATGCTCAGCTAAAAAAGCAACAGTGGAGAAATGCCGTAACTTTT	2474
Db	2556	AGCTTTTAAATAGCTTTTAAAAAGATGCAACCATGGAGAAAATGAATCTATTT	25497

QY	2475	TCTATTACTATGACGCGCTCTTCTGCTTCCCTGACGACAGGAATTAATATATACAT	2534
Db	25496	TGTACTTACCCACAGATTTCTACTTAATTCATTAGATAGAAATTTCCAATATATACAA	25497

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QY      2535 AAATAGAGATATA 2547
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Db      25436 AGATAGAAAGATA 25424

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Search completed: May 23, 2006, 02:08:16
Job time : 35 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2006, 21:42:05 ; Search time 2702 Seconds
(without alignments)
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Title: US-09-419-679-5
Perfect score: 2560
Sequence: 1 tggccttcgagcagcaaa.....agatataaaaaaaaaaaaaa 2560

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues
Total number of hits satisfying chosen parameters: 37784340

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Post-processing: Minimum Match 0%
Maximum Match 100%
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Database : Published Applications NA Main:*

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13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
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16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2560	100.0	2560	US-10-607-726-5	Sequence 5, Appl1
2	1405	54.9	2280	US-09-938-842A-833	Sequence 833, App
3	1405	54.9	2280	US-09-938-842A-833	Sequence 833, App
4	1222	47.7	4120	US-10-437-963-71137	Sequence 71137, A
5	1197.2	46.8	2776	US-10-425-115-91064	Sequence 91064, A
6	1196.2	46.7	2638	US-10-425-114-25096	Sequence 25096, A
7	1196.2	46.7	2786	US-10-425-115-90182	Sequence 90182, A
8	1183.6	45.4	2558	US-10-607-726-1	Sequence 1, Appl1
9	1162	45.4	2355	US-10-437-963-71159	Sequence 71159, A
10	1145.6	44.7	2653	US-10-425-114-24593	Sequence 24593, A
11	944.2	36.9	2478	US-10-421-074-3	Sequence 3, Appl1
12	944.2	36.9	2478	US-10-427-570A-4	Sequence 4, Appl1
13	944.2	36.9	2478	US-11-076-733-18	Sequence 18, Appl1
14	944.2	36.9	2669	US-10-424-599-35539	Sequence 35539, A
15	944	36.8	1882	US-10-607-726-3	Sequence 3, Appl1
16	942.6	36.8	2567	US-10-425-114-7892	Sequence 7892, App
17	917.6	35.8	2593	US-10-425-114-24645	Sequence 24645, A

18	917.6	35.8	2627	9	US-10-425-115-65768	Sequence 65768, A
19	917.4	35.8	2271	16	US-11-096-568A-30648	Sequence 30648, A
20	914.4	35.7	2545	16	US-11-096-568A-24178	Sequence 24178, A
21	914.4	35.7	2574	9	US-10-739-930-2894	Sequence 2894, App
22	905	35.4	2731	7	US-10-221-074-1	Sequence 1, Appl1
23	903.8	35.3	2538	7	US-10-221-074-7	Sequence 7, Appl1
24	897.8	35.1	2746	8	US-10-424-599-31007	Sequence 31007, A
25	897.8	35.1	2766	7	US-10-221-074-5	Sequence 5, Appl1
26	897.8	35.1	2766	7	US-10-427-570A-1	Sequence 1, Appl1
27	897.8	35.1	2766	16	US-11-076-733-19	Sequence 19, Appl1
28	847	33.1	2067	7	US-10-429-949-6	Sequence 6, Appl1
29	843.8	33.0	2179	8	US-10-425-114-9157	Sequence 9157, App
30	819.6	32.0	2510	8	US-10-425-114-24639	Sequence 24639, A
31	817.8	31.9	2484	8	US-10-425-114-10317	Sequence 10317, A
32	817.8	31.9	2484	8	US-10-424-559-4661	Sequence 4661, App
33	810	31.6	2526	9	US-10-424-559-44214	Sequence 44214, A
34	804.2	31.4	2416	8	US-10-424-559-35538	Sequence 35538, A
35	796.2	31.1	2093	7	US-10-424-559-139406	Sequence 139406, A
36	793	31.0	2093	7	US-10-259-194A-115	Sequence 115, App
37	787.8	30.8	1939	8	US-10-425-114-10363	Sequence 10363, A
38	769.8	30.1	2415	8	US-10-739-930-740	Sequence 740, App
39	766.4	29.9	2457	7	US-10-168-445-14	Sequence 14, Appl1
40	756	29.5	761	8	US-10-425-114-10288	Sequence 10288, A
41	732	28.6	1546	7	US-10-259-194A-548	Sequence 548, App
42	722.2	28.2	2639	8	US-10-389-566-248	Sequence 248, App
43	716	28.0	1729	8	US-10-425-114-10855	Sequence 10855, A
44	695.8	27.2	1842	8	US-10-425-114-10336	Sequence 10336, A
45	677.4	26.5	1869	8	US-10-424-599-53604	Sequence 53604, A

ALIGNMENTS

RESULT 1
US-10-607-726-5
Sequence 5, Application US/10607726
Publication No. US20040121439A1
GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Farnodu, Omolayo O.
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Rafalecki, Antoni
APPLICANT: McGonigle, Brian
TITLE OF INVENTION: Enzymes Involved in Squalene Metabolism
FILE REFERENCE: B1113 US NA
CURRENT APPLICATION NUMBER: US/10/607,726
CURRENT FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: US/09/419,679
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/105,405
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Microsoft Office 97
SEQ ID NO 5
LENGTH: 2560
TYPE: DNA
ORGANISM: Glycine max
US-10-607-726-5
Query Match 100.0%; Score 2560; DB 8; Length 2560;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGCCTTCGAGCAAAAGCAATGTGAGGCTCAAGTTGCCGAGAGGAATCCA 60
DB 1 TGGCCTTCGAGCAAAAGCAATGTGAGGCTCAAGTTGCCGAGAGGAATCCA 60
QY 61 TGGCCTTCGAGCAATGAAATCAATCGTTGGAAGACAGGTGTGAGGTTGATCTTAAGCTT 120
DB 61 TGGCCTTCGAGCAATGAAATCAATCGTTGGAAGACAGGTGTGAGGAGTTGATCTTAAGCTT 120

121 GGATGCGCGAAGATCTCTCGAGATTGAGAAAGTCGCGAAGATTTTTCAGCATACCGC 180
Db GGATGCGCGAAGATCTCTCGAGATTGAGAAAGTCGCGAAGATTTTTCAGCATACCGC 180
Qy TTTTACCACAAACACAGGCTGATCTACTATATGCGGATGCAATTGGCAAGAGAACCA 240
Db TTTTACCACAAACACAGGCTGATCTACTATATGCGGATGCAAGAGAGAACCA 240
Qy ACAGGTGAAGTCTTGCCCAAGTCGAGTTAGATATTTAGAGATGTGACCCAAAGATT 300
Db ACAGGTGAAGTCTTGCCCAAGTCGAGTTAGATATTTAGAGATGTGACCCAAAGATT 300
Qy GTGACAAAACATTAAGAAAGGCGTAAGTTTCAATCACTTCAGTCCATGACGGA 360
Db GTGACAAAACATTAAGAAAGGCGTAAGTTTCAATCACTTCAGTCCATGACGGA 360
Qy CACTGGCGGGAGATTATGAGAGTCCCATGTTTCTGATGCTGCTGGTTGTAATCTCTG 420
Db CACTGGCGGGAGATTATGAGAGTCCCATGTTTCTGATGCTGCTGGTTGTAATCTCTG 420
Qy TCTATCACTGGGGCGTTGAATACAGTCTTAACGTAAAGAACATAGAAAGAAATATGCCGT 480
Db TCTATCACTGGGGCGTTGAATACAGTCTTAACGTAAAGAACATAGAAAGAAATATGCCGT 480
Qy TACCTCTATTAATCATCAAAACAAAGAGATGAGTGGGTTTGCCATATTTGAAAGTCCAAAC 540
Db TACCTCTATTAATCATCAAAACAAAGAGATGAGTGGGTTTGCCATATTTGAAAGTCCAAAC 540
Qy ACCATGTTTGGCTCTGTCTTGATTAATTAATCTGAGATTGCTAGAGGAGGCTTAAT 600
Db ACCATGTTTGGCTCTGTCTTGATTAATTAATCTGAGATTGCTAGAGGAGGCTTAAT 600
Qy GATGGAACAAGGGGAATGGAAGAGGCGAGTGAATGATGATGATGATGATGATGATGATGAT 660
Db GATGGAACAAGGGGAATGGAAGAGGCGAGTGAATGATGATGATGATGATGATGATGATGAT 660
Qy TATATTAAGTCACTGAGGGGAAGATGAGTCTTCACTGAGTGTATGAAATGATGATGATGAT 720
Db TATATTAAGTCACTGAGGGGAAGATGAGTCTTCACTGAGTGTATGAAATGATGATGATGAT 720
Qy TATATTAAGTCACTGAGGGGAAGATGAGTCTTCACTGAGTGTATGAAATGATGATGATGAT 780
Db TATATTAAGTCACTGAGGGGAAGATGAGTCTTCACTGAGTGTATGAAATGATGATGATGAT 780
Qy TATATTAAGTCACTGAGGGGAAGATGAGTCTTCACTGAGTGTATGAAATGATGATGATGAT 840
Db TATATTAAGTCACTGAGGGGAAGATGAGTCTTCACTGAGTGTATGAAATGATGATGATGAT 840
Qy TATATTAAGTCACTGAGGGGAAGATGAGTCTTCACTGAGTGTATGAAATGATGATGATGAT 900
Db TATATTAAGTCACTGAGGGGAAGATGAGTCTTCACTGAGTGTATGAAATGATGATGATGAT 900
Qy TATATTAAGTCACTGAGGGGAAGATGAGTCTTCACTGAGTGTATGAAATGATGATGATGAT 960
Db TATATTAAGTCACTGAGGGGAAGATGAGTCTTCACTGAGTGTATGAAATGATGATGATGAT 960
Qy TATATTAAGTCACTGAGGGGAAGATGAGTCTTCACTGAGTGTATGAAATGATGATGATGAT 1020
Db TATATTAAGTCACTGAGGGGAAGATGAGTCTTCACTGAGTGTATGAAATGATGATGATGAT 1020
Qy TATATTAAGTCACTGAGGGGAAGATGAGTCTTCACTGAGTGTATGAAATGATGATGATGAT 1080
Db TATATTAAGTCACTGAGGGGAAGATGAGTCTTCACTGAGTGTATGAAATGATGATGATGAT 1080
Qy TATATTAAGTCACTGAGGGGAAGATGAGTCTTCACTGAGTGTATGAAATGATGATGATGAT 1140
Db TATATTAAGTCACTGAGGGGAAGATGAGTCTTCACTGAGTGTATGAAATGATGATGATGAT 1140
Qy TATATTAAGTCACTGAGGGGAAGATGAGTCTTCACTGAGTGTATGAAATGATGATGATGAT 1200
Db TATATTAAGTCACTGAGGGGAAGATGAGTCTTCACTGAGTGTATGAAATGATGATGATGAT 1200
Qy TATATTAAGTCACTGAGGGGAAGATGAGTCTTCACTGAGTGTATGAAATGATGATGATGAT 1260
Db TATATTAAGTCACTGAGGGGAAGATGAGTCTTCACTGAGTGTATGAAATGATGATGATGAT 1260

1201 AGAATTTATGATTTATCTATGGAATGCAAGAGATGCGATGAAAATGCAAGGCTTACATGGA 1260
Qy AGAATTTATGATTTATCTATGGAATGCAAGAGATGCGATGAAAATGCAAGGCTTACATGGA 1260
Db AGAATTTATGATTTATCTATGGAATGCAAGAGATGCGATGAAAATGCAAGGCTTACATGGA 1260
Qy AGTCAACTATGAGGACACTGCTTTTGTGCTCCAGCATTTTATGATCTTACATGGA 1320
Db AGTCAACTATGAGGACACTGCTTTTGTGCTCCAGCATTTTATGATCTTACATGGA 1320
Qy GAATTTGGTCCCACTATAGAAAAGCTCATACCTATATTAAGATTTTCAAGTTTTGA 1380
Db GAATTTGGTCCCACTATAGAAAAGCTCATACCTATATTAAGATTTTCAAGTTTTGA 1380
Qy GATTTGTCAGGTGATCTTAAATTAATGATGATGATGATGATGATGATGATGATGATGAT 1440
Db GATTTGTCAGGTGATCTTAAATTAATGATGATGATGATGATGATGATGATGATGATGAT 1440
Qy TCAATGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
Db TCAATGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
Qy CTATTTACTATCCAAATTTGCAACGAAATAGTTGATGATGATGATGATGATGATGATGAT 1560
Db CTATTTACTATCCAAATTTGCAACGAAATAGTTGATGATGATGATGATGATGATGATGAT 1560
Qy TATGATTTCTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
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Qy GAGCTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
Db GAGCTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
Qy ATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
Db ATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
Qy TTTAGAAATTAATTCCTGAGCATGCGCGAAGAAATTAACAATGATGATGATGATGATGAT 1800
Db TTTAGAAATTAATTCCTGAGCATGCGCGAAGAAATTAACAATGATGATGATGATGATGAT 1800
Qy ACTTACCTTCAATGAAAATTAACAAGCTTCAAGTATGATGATGATGATGATGATGATGAT 1860
Db ACTTACCTTCAATGAAAATTAACAAGCTTCAAGTATGATGATGATGATGATGATGATGAT 1860
Qy TGTCTTCACTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
Db TGTCTTCACTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
Qy TGTCTTCACTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
Db TGTCTTCACTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
Qy TGTCTTCACTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040
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Qy TGTCTTCACTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2100
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Qy TGTCTTCACTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
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Qy TGTCTTCACTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
Db TGTCTTCACTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
Qy TGTCTTCACTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340
Db TGTCTTCACTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340


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Qy 1465 ATTCTGACGTGACAGCTGAAAGACTGAAAGCTGTTCTATTACTATCCAAAATTCACCA 1524
Db 1441 ATCTGTGACGTGACCGGAGAAAGACTGAAAGCTGCTTTTGTCTATCCAAAGTCCCAAG 1500
Qy 1525 GAAATGTTGGTGGACCAATAGAGTGAAGGATTATATGATTCTGTAAATGTCATTCTC 1584
Db 1501 GCGATTGTTGGTGAACCAATAGATGCAAAACGGTTATGAAAGCTGTAAATGATATCAT 1560
Qy 1585 TCACATGAGAAATGAAAGATGTGTGTTTGGCAACATATAGAGCTTAAACGATCTTATATG 1644
Db 1551 TCTTTACGAATGACGATGAGAGGCTCGCAACATATAGCTCACCAAGTCAATCCCTTGG 1620
Qy 1645 TTGAGATATATCAATCTGCTGAAAACCTTTGGTGCATCGTTATGATTAATCTTANG 1704
Db 1621 TTAGAGCTATATCAACCCAGCAGAAAACCTTTGGCGATATTTGATTAATGATTAATCT 1680
Qy 1705 GAAATGATCATGACGAGCATTCAGCTTTGGCATATTTAGAAATTAATTCCTGGGAT 1764
Db 1681 GAAATGATCATGACGCTATCCAAAGCTTTGATATCATTTGAAAGCTGTATCTGTGAT 1740
Qy 1765 GCGCGAAGAAATATCAACATTTGATGATAAGCCATACCTTCATTTGAAAATAACAA 1824
Db 1741 CGAAAGAGAAAGATGATGATGATGCTTGAAGAGCGGTTAAAGTTCATTGAATCCATCA 1800
Qy 1825 GCTTCAGATGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1884
Db 1801 GCAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
Qy 1885 GGGGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1944
Db 1861 GGAAGTAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
Qy 1945 GCTTGTGATTTTCTGCTGCTGCAAGAGCTTCCTTGTGCTGGGAGAGAGATTAATCTG 2004
Db 1921 GCTTGTGATTTTCTGCTGCTGCAAGAGCTTCCTTGTGCTGGGAGAGAGATTAATCTG 1980
Qy 2005 TCCTGTCAAAAACAAGTGTATTAATCTGAAAGGCAACAGTCTCATGTGTCAACA 2064
Db 1981 TCATGTCAAGAACAAAGTGTATTAATCTGAAAGGCAACAGTCTCATGTGTCAACA 2040
Qy 2065 GGGTGGGCTATGTTGGCTCTCATTTGATGATGATGATGATGATGATGATGATGATGAT 2124
Db 2041 GCATGGGCTATGCTGCACTCATTTGCTGCTGGCAAGCTGAGTGAACCGGAAACCACTA 2100
Qy 2125 CACGGGAGCTGCACTATCTGATTAATCCCAATTTGAGAGCGGATCTTCGAGAG 2184
Db 2101 CACGGGCTGCAAGATCTTGTATTAATCTGCAATGAGAAATGATGATTTTCCACACAG 2160
Qy 2185 GAAATATGAGAGTCTTCAACAAGATTTGATGATGATGATGATGATGATGATGATGATGAT 2244
Db 2161 GAAATATGAGAGTCTTCAATGAGAACTGCAATGATTAATGATGATGATGATGATGATGAT 2220
Qy 2245 TTCCCATTTGGGCTTGGGAGATACCAATCCCAAGATTT 2285
Db 2221 TTCCGATATGAGGCTTTGGGAGAGTACCGTGTGTGATGATTT 2261

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RESULT 3
US-09-938-842A-833

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; Sequence 833, Application US/0938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SRIPI300-3
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2000-08-24

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; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 833
; LENGTH: 2280
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-833

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Query Match 54.9%; Score 1405; DB 3; Length 2280;
Best Local Similarity 76.3%; Pred. No. 0;
Matches 1726; Conservative 0; Mismatches 535; Indels 0; Gaps 0;

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Qy 25 ATGTGAAAGCTCAAGTTGCGCGAAGAGGGAATCCATGCTTGGACATTTGAACATATCAC 84
Db 1 ATGTGAAAGCTCAAGTTGCGCGAAGAGGTAATGTCATGAGTCAAGAACACCAATATATCAC 60
Qy 85 GTTGAAGACAGGTGTGGAGTTCGATCTTAAGCTTGGATCGCCGCAAGATCTCTCGAG 144
Db 61 GTCGAAGACAGTTTGGAGTTCGATCTCGATCTCGTATCTCTGAGATCTTCGCCGCC 120
Qy 145 ATTGAGAACTCGCCAGAAATTTTACGATTAACCGCTTTACCAAAACACAGCGTGAT 204
Db 121 GTCGAAGAACTCGAAGTCTTTTTCGATTAATGATTCGTGCAAGAAACATAGCGCGAT 180
Qy 205 CTACTTATGCGGATGCGATTCGCAAGAGAACCAACAGTGAAGCTTGGCCAAAGTC 264
Db 181 CTGCTTATGCGCTTCAGTTTTCAGAGAAATTTGATTAGCCAGTTTATCTCAAGTTC 240
Qy 265 GGAATTAAAGATATTGAGATGATGACCAAGATTTGTGCAAAAACATTAAGAAAGGCC 324
Db 241 AAATGAAAGACATGATGATGATTAAGAGAGATGTTGAAACCAAGTAAAGAGGGGT 300
Qy 325 GTTAATTCATTAACCTTCAGTGCATGACGAGACATGCGCGGAGATTAATGAGGT 384
Db 301 CTAGATTTCTATTAACATATACAGGACACAGAGCGGACATGCGGAGTATGATGATGAT 360
Qy 385 CCAATGTTTCTGATGCTGCTGCTGTTAATTAATCTGCTATCACTGCGGGGTTGAATACA 444
Db 361 CTAATGTTTCTTCCAGGACGATTAATTAATCTCTCAATTAACAGGACATGAATACA 420
Qy 445 GTCTTAAGTAAAGACATTAAGAAAGAAATATGCGGTTAATCTCTTAATCAATCAAAACAG 504
Db 421 GTATGTCGAGAACATTAAGAAAGAAATGCGCGGTTATCTCTTAATCAACGAAATGAG 480
Qy 505 GATGTGGTGGGCTTTCATATTTGAAGTCCAGACCAATGTTGGCTGTCTTGATGAT 564
Db 481 GACGAGGTTGGGCTTTCATATTTGAAGGCGCTTACGACCAATGTTGGCTGTCTTGATGAT 540
Qy 565 TATATTAATCTGAGATTCGATGAGTGAAGGCGCTTAATGATGAAGGAGAAAGGAGAG 624
Db 541 TATGTTACTTAAGTGTCTTGAAGAGGACCTTAACGATGAAGATGATGAAGAGAA 600
Qy 625 GCAAGTACGATTTCTAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 684
Db 601 GAGAGACCTGATTAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Qy 685 TGGCTTCAAGTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 744
Db 661 TGGCTTCAAGTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Qy 745 TGGCTTCAAGTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 804
Db 721 TGGCTTCAAGTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Qy 805 GTCTATTTGCGAGTCTCTAATATGAGCAAGGTTTGTGATGATGATGATGATGATGATGATGAT 864
Db 781 GTGATCTTGGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Qy 865 GTATTAATCTTGAAGAAAGCTTTTATACAGTACCAATACATGATTAATGATGATGATGATGAT 924

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Db 841 GTTTTATCATGAGAAAGAGCTTTTCAAGTACCATATCATGAAGTCAAGTGAATGA 900
 Qy 925 GCTGCAATTTGTGTGCAAAAGAAATTTGATCTTCAACCCACTTGTATCAAGATATT 984
 Db 901 GCAACCAACCTTTGGCGAAAGAGATTTATCTACCCACATCCACTTGTGCAAAATATT 960
 Qy 985 CTTTGGGCACTCTTACACAAGTTCCTTGGAGCTTATTCGATGCAATTTGGCTGAAAAGAA 1044
 Db 961 CTTTGGGCACTCTTACACAAGTTCCTTGGAGCTTATTCGATGCAATTTGGCTGAAAAGAA 1020
 Qy 1045 TTGAGGAAAGAGCTATTATTTCTGCAATGGAGCATATACATTAGCAAGATGAAATCT 1104
 Db 1021 TTGAGGAAAGAGCTATTATTTGAAACCGCAATGAAACATTTATGAAATGAAATATCT 1080
 Qy 1105 CGATATATTGCAATAGCTCTGTAAATAGGTGTTAAATATGCTTGTGCTGGTGGAA 1164
 Db 1081 AGTACATCTGATAGTCCCGTGAAACAAGTATTAATATGCTTGTGCTGGTGGAA 1140
 Qy 1165 GATCCAAATTCGAGGCTTCAAGTTCGATCTCCAGAGATTTATGATATCATGATGAT 1224
 Db 1141 GACCCAACTCAGAGGCTTTCAGATTCACCTACCAAGAAATCATGACTTTCCTGGTTA 1200
 Qy 1225 GGAAGAGATGAGCTGAAAGATGAGGCTACATGAAAGTCAACTATGAGCACTGCTTT 1284
 Db 1201 GCTGAAGATGAAATGAAATGAGGCTTATTAACGAAAGCACTATGGAATACAGTTT 1260
 Qy 1285 GCTGTCCAAAGCAATTTATGATCTTCACTTGAAGAAATTTGCTCAATATGAAAGAA 1344
 Db 1261 GCTATTCAGAGCAATTTTGGCAATTAATCTGCTGAAAGAAATATGGCCGCTTTGAAAGAA 1320
 Qy 1345 GCTCATACCTATTATTAAGATTCACAGGTTTGAAGATTTGCTGAGTATCTTAATAA 1404
 Db 1321 GCACATTCATTTGTCAAGAAATTCACAGGTTTGAAGATTCGCTGAGATTCGAATTC 1380
 Qy 1405 TGGTACCGTCACTTTCAAAAGGCTGGCTTTTCAACTGAGATCATGATGAGCA 1464
 Db 1381 TGGTATCGCACTTTCAAAAGGCTGGCTTTTCAACTGAGATCATGATGAGCA 1440
 Qy 1465 ATTTGCACTGCAAGCTGAGAGCACTGAAAGCTGTTCTATTAATTCAAATTCAGCA 1524
 Db 1441 ATCTGCACTGCAAGCTGAGAGCACTGAAAGCTGTTTGTATTCAAAGTTCAGCA 1500
 Qy 1525 GAAATAGTGTGAGAGCAATGAGCTGAGAGCAATTAATGATCTGTAATGCTATTC 1584
 Db 1501 GCGATTTGTGTAACCAATAGATGCAAAACGCTTATATGATGATGATGATTCAT 1560
 Qy 1585 TCACTACAGAAATGAGTGTGTTTGGCAATATGAGCTTAAAGATTTAATTTG 1644
 Db 1561 TCTTTACAGAAATGAGTGTGTTTGGCAATATGAGCTTAAAGATTTAATTTG 1620
 Qy 1645 TTGGAATATCATCTGCTGAAACCTTTGAGCACTGTTATGATTTATCTTATG 1704
 Db 1621 TTGGAATATCATCTGCTGAAACCTTTGAGCACTGTTATGATTTATCTTATG 1680
 Qy 1705 GAAATATCATCAGAGGATTCAGCTTTGCAATGATTAAGAAATTAATTCCTGGCAT 1764
 Db 1681 GAAATATCATCAGAGGATTCAGCTTTGATTAATGATTAATTCCTGGCAT 1740
 Qy 1765 GCGGAGAGAAATTAACAATTTGATGATTAAGAGCACTACCTTATGAAAGAAATTA 1824
 Db 1741 CGAAAGAGAGAAATGATGATGATTAAGAGCACTACCTTATGATTAATTCAT 1800
 Qy 1825 GCTTCAAGATGATCATGATGATGATTTTGGGAGATTTGCTTCACTTACGCTGCTG 1884
 Db 1801 GCAAGCAATGCTATGATGATGATTTGAGCTGCTTCACTTACGCTGCTGCTG 1860
 Qy 1885 GGGGTAAAGGCTGATGCTGCTGAGAGAGTTCAATGATGCTCAAGCATCCGTA 1944
 Db 1861 GAGGTAAAGGCTGATGCTGAGAGAGTTCAATGATGCTCAAGCATCCGTA 1920
 Qy 1945 GCTTGTGATTTTCTGCTGCTGAGAGAGCTTCTTGTGCTGCTGAGAGAGATTA 2004
 Db 1921 GCTTGTGATTTTCTGCTGCTGAGAGAGCTTCTTGTGCTGCTGAGAGAGATTA 1980

Qy 2005 TCTGTCAAAACAAGTGTATTTCAATCTGGAAGCAACAGTCTCATGTGTCAACCT 2064
 Db 1981 TCAATCAAGCAAGTCTTATTTCAACCTTATGGAACAAGATCTCAGCTGTGAATCA 2040
 Qy 2065 GGGTGGCTATGTTGGCTCTCATTTGATGCTGAGCAAGCTTAAGAGATTTGCCAACATG 2124
 Db 2041 GCATGGCTATGCTGCACTCATTTGCTGTGGGCAAGCTGAGTGAACCGGAAACACTA 2100
 Qy 2125 CACGGGCACTGCACTTTTGAATTTCCCAATTTGAGGAGCGGTACTTCCGAGCAG 2184
 Db 2101 CACGGGCTGCAAGTACTTGAATTTATGCTCAAAATGGAATGGATTTTCACACAG 2160
 Qy 2185 GAAATATGAGGAGCTTCAACAAGATTCATGATCATATGCGCGCATACAGAAACATA 2244
 Db 2161 GAAATATGAGGAGCTTCAATGAGAACTGATGATTAATGCGGCTATCGAAACATT 2220
 Qy 2245 TTCCCATTTTGGCGCTTGGAGAAATACCAATCCCAATATT 2285
 Db 2221 TTTCGATATGGGCTTTGGGGAGTACCGTTGTGATATT 2261

RESULT 4
 US-10-437-963-71137
 ; Sequence 71137, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Bardazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 71137
 ; LENGTH: 4120
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_7163C.1
 US-10-437-963-71137

Query Match 47.7%; Score 1222; DB 8; Length 4120;
 Best Local Similarity 71.6%; Pred. No. 0;
 Matches 1603; Conservative 0; Mismatches 635; Indels 0; Gaps 0;
 Qy 49 GAGGGAATCCATGCTGCTGGAATTCAGCAATTCAGTGAAGAGAGAGAGTTC 108
 Db 23 GGGGGGAGCCCGTGGCTGCGACGAAAGAGGCACTGAGGCGCAGGCTGGAGTT 82
 Qy 109 GATCTAAGCTTGGATGCGCGCAAGATCTCTGAGATTTGAGAAAGCTGCCAGATTT 168
 Db 83 GACCCGCGCGGCGAGACCCCGAGAGCTGCGCGCGTGAAGGCGCGCGCGGTTTC 142
 Qy 169 CACGATACCGCTTTTACCAACAACAGAGCTGATCTTATATGAGATGAGTTCGA 228
 Db 143 GCGGCGCGCGCAGCAGAGCTCAAGCAACACTCGACCTCTCATGCGAGTGGCT 202
 Qy 229 AGAGAGAACCAACAGTGAAGTCTTCCCAAGTGGAGTTAAGATATTGAGATG 288
 Db 203 AAGCAAAATCTTTAAGCTGAGCAATTCAGCTATCAAGCTAGAGAGAGATGAGCT 262
 Qy 289 ACCCAAGATTTGTGCAAAACATTAAGAGAGGCGTGAAGTTCCATTCAACTTCAG 348
 Db 263 ACAGGGAAGCTGTATTATCTCTTAAAGAGGCAATGCTGTTATTTCTACTTTCAA 322

349 TGCATGACGACATGCGCCGGAGATTATGAGGCTCCATGTTCTGATGCTGGCTTG 408
323 GCACATGATGACATCTGGCTTGGGGATTATGGTGGTCCCATGTTCTTATGCGAGGCTTG 382
409 GTAATTACTCTGTCTATCACTGGGGCTTGAATACAGTCTTACTGAAGAACTATGAAG 468
383 ATTATMACTATTATGTGAGCGGACGCTGAACACCTGCTTGTCTATCGAACATCAGAA 442
469 GAATATGCGCTTACTCTATATATCATCAAAACAAGATGGTGGGTGGGGTTTGCAATT 528
443 GAGATACGGCGGTATCTTACATATCATAGATGAAGATGAGAGATGGGGTTTGCAATT 502
529 GAAGGTCCAAAGCACCATGTTGGCTCTGTCTTGAATTATTAATCTCTGAGATGGTAGGT 588
503 GAGGGCCACAGCACAATGTTGGCTCAGGTTGAATATGTTTCTTTGAGATGGTTGG 562
589 GAGGGGCTTATGATGACAAAGGGAAATGAGAAAGCACTGACTGATCTAGGGCAT 648
563 GAGGGGCCAGATGCGCGGATGAGCTATGAGAAAGACGAAATGATTTTGAACCAT 622
649 GGTGTGCTACTTATATATACGTCATGAGGGGAAAGATGGTCTTCACTTGAAGTAT 708
623 GGGGAGCAACTTATATTAATCATCATGAGGGCAAGTTTGGCTTGGTCTGCTGCTATTT 682
709 GAATGCTCTGAAATATATCCCTGCGCCCTGAGATATGCTCTTCAATACATGCTTCA 768
683 GACTGTCTGGCAACACCACTGCTCACCAGAAATATGGTTGTTGCCATATTTCTGCG 742
769 TTTTATCCAGAGAGATGTTGTGTCATGCGGATGCTATTTTGGCCGATCTCTATTA 828
743 ATTCATCCAGGGCGAATGTTGTGTCATGCGGATGCTTATTTGCTATGTTTACAT 802
829 TATGCAAGAGGTTTGTGTCATCTCAATCTCAACCAAGATTAATCTTGAAGAAAGATT 888
803 TATGAAAGAGGTTTGTGTCAGTACCACTATTAATGAAATTAAGAAAGAACTC 862
889 TATACAGTACCATACCATATATATGATTTGAGTACGCTCCGATTTTGTGCAAGAA 948
863 TACGAATGATCCCTTACATGAAATGATTTGGACAAAGGCTCCGATCTATGTCCTA 922
949 GATTTGATCTATCTCACCACCTTGTACAGATATCTTTGGGATCTCTACAAAGTTC 1008
923 GATCTGATCTATCCATCTCATTCATTCGTGAGAGATGATTAATGGCCATCTCCAAATTT 982
1009 CTGAGGCTATTTCTGATGATGCTGGCTGGAAAAAATTTGAAGGAAAGCTATTTCT 1068
983 GTTGAACCAAGCTATGTCGTGGCTGGGAAACAATTTGAAGGAAAGCTTTGACACT 1042
1069 GCATTGAGCATATATCATTAACGAAGATGAAATCTCGATATATTTGATAGTCTCTGA 1128
1043 GTCATGACGATATTTCAATTAAGATGAAACACCCGATATATTTGATGTTGCTCA 1102
1129 AATAAGGTATTAATATGCTTGTGCTGTTGGTGAAGATCCAAATTTGAGGCTTCAAG 1188
1103 AACAAAGTATTAATATGCTTGTGCTGATGTAAGATCCAAATCTCAGAGCAATTC 1162
1189 TTGATCTTCCAGAGATTTATGATATCTATGATTTGCAAGATGAGATGAAAAATG 1248
1163 CTCACATTTCCAGAGATCCAGATTAATCTATGATTTGCAAGAGATGAAATGAG 1222
1249 GAGTCAATGAGAGTCAATTAATGAGCACTGCTTGTGCTGTCAGCAATTAATGATCT 1308
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1309 AACCTCATTTGAAGATTTGCTCAACTATTAAGAAAGCTCATCTATATTAAGATTTCA 1368
1283 GGCCTCATTTGAAGATTTGCTCTACTTAACTAGACATGCTTATTAAGAAAGAAAG 1342
1369 CAGGTTTGAAGATTTGCTCAGGATCTTAAATTAATGATGATCCGTCATTTCAAGGT 1428
1343 CAGGTTTATGATGATGCTCCGAGATCTTATGATGATGATGATGATGATGATGAT 1402
1429 GCTTGGCTTTTCAACTGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1488

1403 GCATGCGCTTTTCTACTGCTGATCATGTTGGCTTATTCAGATTCATGCAAGAA 1462
1489 CTGAAGAGTGTCTATTAATTAATCAAAATTTGACACCAAAATATGTTGGTGAAGCAATGAC 1548
1463 CTTAAGGCGGATTAATGCTATGAGAAATTTCTCAGATATGTTGGCGAAAGCTGGA 1522
1549 GTGAAGGATTAATTAATGATTTGTAATGATGATCTCTCAGTACAGATGAAGATGTTGT 1608
1523 GTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1582
1609 TTTGCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1668
1583 TTTGCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1642
1669 ACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1728
1643 ACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1702
1729 GCTTGGATCATTTAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1788
1703 GCTTGGATCATTTAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1762
1789 ATGATTAAGGCACTTATCATTTGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1848
1763 ATAGCAAGAGTGTGATCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1822
1849 TCTTGGGAGATTTGCTTCACTTACATGATGATGATGATGATGATGATGATGATGATGAT 1908
1823 TCTTGGGAGATTTGCTTCACTTACATGATGATGATGATGATGATGATGATGATGATGAT 1882
1909 GGAAGAGATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1968
1883 GGTAGGATTTCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1942
1969 CAGTCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2028
1943 GAGCTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2002
2029 AATGGAAGGCAAGATCTCATGATGATGATGATGATGATGATGATGATGATGATGAT 2088
2003 AATGGAAGGCAAGATCTCATGATGATGATGATGATGATGATGATGATGATGATGAT 2062
2089 GATGCTGACAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2148
2063 GATGCTGACAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2122
2149 AATCCCAATTTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2208
2123 AACTTACAAATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2182
2209 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2268
2183 AACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2242
2269 TACCAATCCCAAGATG 2286
2243 TACCGTCGCGGCTTG 2260

RESULT 5
US-10-425-115-91064
; Sequence 91064, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: Ia Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115


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? CURRENT FILING DATE: 2003-04-28
? NUMBER OF SEO ID NOS: 369326
? SEO ID NO 91064
? LENGTH: 2776
? TYPE: DNA
? ORGANISM: Zea mays
? FEATURE:
? OTHER INFORMATION: clone ID: MRT4577_183051C.1
? US-10-425-115-91064

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Query Match	46.8%	Score	1197.2	DB 9	Length	2776
Best Local Similarity	71.2%	Pred. No.	0			
Matches 1599	Conservative	0	Mismatches	638	Indels	9
					Gaps	1

Oy	49	GAAGGAATTCATGGCTTCGGACATTGAAACAATACGTTGGAAACAAGGTGGGAATTC	108
Db	229	GGCGGGACCCCTGGCTCCGACCAAGAACGCCCACTCGGCGCGCAGGTCTGGGAATTC	288
Oy	109	GATCTTAAGCTTGGATCGCCGCAAGATCTCCTGAGATTGAAAAGCTCGCAGAAATTTT	168
Db	289	GAGCGC-----TCGGCCGACCCCGACCCCCCGCTCGACGCGCGCGCGCTTC	339
Oy	169	CACGATTAACCGCTTAACCCAAACACAGGCGCTATCTACTTAAGCGGATGCGAATTCGA	228
Db	340	GCCGCGACAGAGGGGCACTTCAAGACAGCGGCCACCTCTCAAGCGCATCAATTTGCC	399
Oy	229	AGAGGAACCCCAACAGTGAAGTCTTGCGCCAAAGTCGAGATTGAAGATTAATGAGATGTG	288
Db	400	AAAGAAATTCCTTTGAGCTTGACCTTCACAGCATCAAGCTCGGTGAGCAAGAAAGTA	459
Oy	289	ACCCAGAGATTGTGACAAAAATTAAAGAGCGCGTAAGTTTCATTCACTCTCCAG	348
Db	460	ACCGGAGAGCGGTGTCTACTACTTTGAAAGGGCGCAATCAGCCGTCCTTACTCTCAG	519
Oy	349	TGCCATGACGACACTGGCGGGAGATTATGAGAGTCCCATGTTTCTGATGCTCGGCTTG	408
Db	520	GCACTATATGACACTGGCTCGGGGATTATGATGCGCTTATGTTCTTATGCCAGGCTTG	579
Oy	409	GTAATTACTCTGTCTACTCTGGGGCGTTGAATACAGTCTTAAGTGAAGACATAGAAG	468
Db	580	ATCATTAATTTGATGTAGCTGAGACATAAACACTGCTCTGTATCAGAACACAGAAAG	639
Oy	469	GAATATAGCGGTAACTCTATATATCATTAACAAGAATGGTGGTGGGGTTTGCAATT	528
Db	640	GAGATCCGTGCTATCTTTATATATCATAGAATGAATGATGTGCTGGGGCTTGCAATT	699
Oy	529	GAAGTCCAGACCACTTTGGCTCTGTCTTGAGTTATTAATCTGAGATTGCTAGT	588
Db	700	GAGGTCCAAGACCATATTTGGCTCAGACATGACCTAAGCTTAATTGAGATTGCTTGA	759
Oy	589	GAGGGGCTTAATGATGACAAAGGGGAAATGGAAGGCACTGACTGATTTCTAGGGCAT	648
Db	760	GAGGACCAAGATAGTGAGATGAGCAATGAGAAAGGCCAATACTGATCTTGAACAT	819
Oy	649	GGTGTGCTACTTATATTAACGTCATGGGGGAAAGATGAGCTTTCAGTACTTGAAGTAT	708
Db	820	GCGGAGCACTATATTAACATCTTGGGGGAAAGTTTGGCTCTCGGATCTTGGGTATTT	879
Oy	709	GAATGCTTGAATTAATCCCTGCGCCCTGAGATATGAGCTCTTCCATACATGCTTCCA	768
Db	880	GAATGCTCTGTATACAAACCGGTAACCAAGAAATATGATCTACATCTCTCGCA	939
Oy	769	TTTTCATCCAGAAAGATGTGTGTCTGACGCGGAGTGTCTAATTTGGCGCATCTCTACTTA	828
Db	940	TTTCAACCAAGGAGATGTGTGTCTAATGTGCAAATGTGTATTTGCCAATGTGTCAATTC	999
Oy	829	TATGCAAGAGGTTTGTGTGTCATCTCACCAACAGATTAATCTTTGAGAAAAGAGCTT	888
Db	1000	TATGGGAAGAGGTTTGTGTGTCATCAACCACTGTTGGAATTAAGAAAGAACTT	1059
Oy	889	TATACAGTACCATACATGATTAATTTGGGATCAGGCTCCCAATTTGTGTCAAAAGAA	948
Db	1060	TTCAAGAGCCCTTACAGCAAGTTATTTGGGCAAGAGCCCGCAATCTATATGTGCTAAGAA	1119

OY	949	GATTGTGATCTACTCTCAACCACTTTGTA CAGATATTTCTTTGGGATCTCTACACAATTC	1008
Db	1120	GATCTGATCTACTACCAATTCATTTGTCAGAGATCTTAATGGGCACTCTCCATTAATTT	1179
OY	1009	CTTAGGCTTATCTCGATGSCATTTGGCCCTGGAAAAAGATTTGAGGGGAAAAAGCTATTAATTTCT	1068
Db	1180	GTTAACCACGTTATGATGATGATTTGGCCCTGGCAGTAAATTTAGAGGAGAAAGCTCTGGACACA	1239
OY	1069	GCATTTGAGCATATATACATTAAGAAATGAGAAATATCTCGATATATTTTGCATAGGTCCTGTA	1128
Db	1240	GGCATGCAACATGTTCTACTATGAGAGTAGAACACTGGTATCAATTTTGCATTTGGCTCTGTA	1299
OY	1129	AATAAGGTGTTAAATATAGCTTTTGTCTGTGGGTGGAATATCCAAATTTGAGGCGCTTCAAG	1188
Db	1300	AACAAGGATTAATTAATATGCTTTCCTTGGATGTGAATCCAAACTAGAGGGCTTTGAAA	1359
OY	1189	TTGATCTTCCACAGATTTTAATGATTAATCTATGATTCAGATTCAGAAAGATGSCATGAATAATCAG	1248
Db	1360	CTCCACATCCACAGATCTATGATCTTATGCTTTGGCTTGTCTGTAAGATGSCATGAAGATCAG	1419
OY	1249	GGCTACATGAGATCAATCAATATGAGCACTGCTTTTGTCTGTCCAGCAATTAATTCATCT	1308
Db	1420	GGCTATATATGTTATGCCAACTTTGGGATATACAGCTTTCAATATGTTCAAGCAATGTGTGATCC	1479
OY	1309	AACCTCATTTGAGAATTTTGTGCCAATATTAAGAAAGCTCATATCTATTAATTAAGATTTCA	1368
Db	1480	AACCTTACCGAAGATTTTGTGTCGCCACCTTAACTACACACAACAATATATCTAACAAGAAATCA	1539
OY	1369	CAGGTTTTAGAAAGATTTGTCCAGGTGATCTTAATTAATGTAACGGTCACTTTGAAAAGGT	1428
Db	1540	CAGGTTCTTTCAGACTGCCCTGGTGATCTGATATACGTGATCCGCCACACATCTTAAAGGC	1599
OY	1429	GCTTGGCCCTTTTCAACGTGAGATCATGAGATGSCCAATTTCTGACTGCACACAGCTGAAGGA	1488
Db	1600	GCATGCGCATTTCTCAACCGGAGATCATAGTGTGGCTATATCTGATTTGCACTGCTGAAGGA	1659
OY	1489	CTGAAGGCTGTCTTATTAATCTATCCAAAATTTGCACAGAATATGTTGGTGAAGCAATAGAC	1548
Db	1660	CTAAAGGCTTCATTAATTTGTTATCAAGAATTTCTCTGAAAATTTGTTGGTGAAGCCGATGAA	1719
OY	1549	GTGAAGCATTTATATGATTTCTGTAAATGTCAATCTCTCACTACAGAATGAAGATGTGTGT	1608
Db	1720	GCTATATGATTTTATGATGTCTGATGTGTCTGATGTCTTAATGAATGAATAAATGGTGT	1779
OY	1609	TTTGGCAATATATGAGCTTAAACGATCTTAATTAATTTGGTGAATATCAATCTGCTGAA	1668
Db	1780	TTTGGCATTTATGAACTCAACAAGATCTTATCTCTGCTGGAGCTGATATCTCTGCTGAG	1839
OY	1669	ACTTTTGTGTGATCTGTTATGATTTATCTTATGTGAAATGTAATCATCAGACGATTCOA	1728
Db	1840	ACCTTTGGGGAATTTGTGATTTGATTAACCGATGTGTAATGTAATCATCAGACGATTCAG	1899
OY	1729	GCTTTGGCATATTTAGGAAATTAATATCTTGGGCATGCGCGAGAAAGAAATCAACATTTGT	1788
Db	1900	GGCCCTGACATCATTCAGAAACTATATCCCTGGGCAACGCAAGAAAGGTGAGCAAACTGT	1959
OY	1789	ATCGATTAAGCATCTACTCTTATTTGAAGAAATTAACAAGTTAGATGATCATATGATATGTGT	1848
Db	1960	ATCAGCAAAAGCTGCTAATTTCTATTTAGAGCAATTCAGAAAAGTGAACGTTCAATGATATGGC	2019
OY	1849	TCTTGGGAGATTTGCTTCACTTACGAGTCTTGGTTTGGGATGAAGAAAGCTCATTTGCTGCT	1908
Db	2020	TCTTGGGCTGTTTGTTCACGTAAGGCACTTGGTTTGTGTGAAAGGACATAATTTGCTGCT	2079
OY	1909	GGAAAGATTTCAATTAATTTGCTCAAGCATCCGTAAGCTTGTGAATTTCTGCTGTCCAAG	1968
Db	2080	GGTAGAATTTTGAAGAGCATGCTGCAATTCAGAAAGGATCCGGCTTTCTGTATCAAAA	2139
OY	1969	CAGCTTCTTCTGTGGGTGGGAGAGATTAATCTGTCTCTCAAAACAAGTGTATTTCA	2028
Db	2140	GAGCTTCTCTTCCGGGTGGGAGAGAAAGCTAATTAATGCTTCAAGACACAGTTTACAC	2199

1116 GATCTGACTACCAACCACTTCGTTCAAGATGTTATGGGCCACTCTCCATTAATTC 1175
1009 CTTGAGCCTATTGCGATTCGCTGCGTGAAGAAAGTTAGAGAAAGGCTATATTCT 1068
1176 GTTAAACAGTTATGATCATTTGGCTGGCAGCAATTTGAGGAGAAAGCTCTGAAACA 1235
1069 GCATTGAGCATATATCATTTAGAGATGAAATACTCATATATTTTGGATGCTCTGTA 1128
1236 GTCAATGCAACATGTTCAATTATGAGAGATGAAACACTCTTATATTTTGGATGCTCTGTA 1235
1129 AATAAGGTTTAAATATGCTTGTCTGTGGGTGAGAAATCCAAATTTGAGGCTTCAAG 1188
1296 AACCAAGATTTGAAATATGCTTGTCTGTGAAATGAAATCCAACTCGAGGCTTCAAA 1355
1189 TTGATCTTCCAGAGATTTATGATTTATGATGAGATTTGAGAAAGATGAGAAATGAG 1248
1356 CTTATATCCCAAGATGATGATTTATGATGAGATTTGAGGATTTGAGAAAGATGAGAG 1415
1249 GAGTACAAATGGAAGTCACTATGAGACATGCTTTTGTCTGATCCAAATTTATTCATCT 1308
1416 GATTATATGCGAGCACTTTGGATACAGCTTTCAAGTTCAAGCATTGTGCTAC 1475
1309 AACCTATTTGAAGATTTGGTCCAACTATTAAGAAAGCTCATCTATATTAAGATTTCA 1368
1476 AACCTATTTGAAGATTTGGTCTTACCTTAACTAGACACAACATATATCAAGATTTCA 1535
1369 CAGGTTTAAAGATTTGTCAGAGTGAATCTTAATTAATGATTCCTGATCAATTTCAAAAGT 1428
1536 CAGGTTCTTGAATGATGCTGCTGAGTATGTAATGATGATGATGATGATGATGATGAT 1595
1429 GCTTGGCTTTTTCACATGAGATCATGATGAGATGAGCAATTTTCTGATGAGTGAAGA 1488
1596 GATATGCAATTCATCACTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1655
1489 CTGAAAGCTTTCTATTAATCAATCAAAATTTGCAACCAAGATTTGATGATGATGATGAT 1548
1566 CTTAAAGGCTCATATTTGATTTCAAGATTTCTCCCAAAATTTGATGATGATGATGATGAT 1715
1549 GTGAAGCATTTATGATTTCTGTAATGATGATGATGATGATGATGATGATGATGATGAT 1608
1716 GCTATATATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1775
1609 TTTGCAACATATGAGCTTAAAGATTTATATATTTGATGATGATGATGATGATGATGATGAT 1668
1776 TTTGCGACATATGAGCTCAAGATTTATATTTGATGATGATGATGATGATGATGATGATGAT 1835
1669 ACTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1728
1836 ACTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1895
1729 GCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1788
1896 GCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1955
1789 ATTCATTAAGCACTATCTTCAATTTGAAATTAATCAAGCTTCAAGATGATGATGATGAT 1848
1956 ATTCAGCAATGCTCAATTTCAATGAGATTTCAAGAAAGCATGATGATGATGATGATGAT 2015
1849 TCTTGGGAGATTTGCTTCACTTACGATGATGATGATGATGATGATGATGATGATGATGAT 1908
2016 TCTTGGGAGATTTGCTTCACTTACGATGATGATGATGATGATGATGATGATGATGATGAT 2075
1909 GAAAGGATTTCAAGTATTTGCTCAAGCATCGGTAAGATTTGATGATGATGATGATGATGAT 1968
2076 GATGAAATTTGAGAAAGTCTGCAATTTGAAAGGATGATGATGATGATGATGATGATGAT 2135
1969 CAGCTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2028
2136 GATCTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2195
2029 AATCTGAAGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2088
2196 AATCTGAAGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2255

2089 GATCTGAGAGGCTAAGAGATTTGCAACACTGAGACCGGAGCTGACTATGATA 2148
2256 GATCAGAGCCAGGCGGAGAGATTCAGCCCTTCAACCGAGAGCAAGGTTTATC 2315
2149 AATTCCCAATTTGAGAGCGGTGACTTTCCGAGAGGAAATTAATGAGATCTTCAACAG 2208
2316 AACTTGCATATCATATGATGAGATTTCTCAGCAAGATCATATGAGATGTTCAACAG 2375
2209 AATTGATGATCATATGAGGCTGATACAGAAATTTCCCATTTGGGCTTGGAGAA 2268
2376 AACTGATGATTAACATCTCCAGTACAGAAATTTCCCATTTGGGCTTGGAGAA 2435
2269 TACCAATCCCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2317
2436 TACCGATGCGAGATTTGGGAGCTTGGAGAGCTTGGAGAGCTTGGAGAGAG 2484

RESULT 8
US-10-607-726-1
Sequence 1, Application US/10607726
Publication No. US20040121439A1
GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Omolayo O.
APPLICANT: Hiez, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Rafalski, Antoni
APPLICANT: McGonigle, Brian
APPLICANT: Lohman, Karin
TITLE OF INVENTION: Enzymes Involved In Squalene Metabolism
FILE REFERENCE: B81113 US NA
CURRENT APPLICATION NUMBER: US/10/607, 726
CURRENT FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: US/09/419, 679
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/105, 405
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Microsoft Office 97
SEQ ID NO 1
LENGTH: 2558
TYPE: DNA
ORGANISM: Zea mays
US-10-607-726-1

Query Match 46.2%; Score 1183.6; DB 8; Length 2558;
Best Local Similarity 72.2%; Pred. No. 1.2e-313;
Matches 1540; Conservative 0; Mismatches 594; Indels 0; Gaps 0;

184 ACCCAAAACAGAGCGCTGATCTTATGCGATGAGATGCGAAGAGAAACCAACA 243
3 ACAGCAAGACAGCGCGACCTCTCATGCGATCAGTTGCGCAAGAAAGTCTGATT 62
244 CGTGAAGCTTTGCCAAGTCGAGATTAAGATTTGAGATGAGACCAAGAGATTTGT 303
63 GAGTTGACCTTCCAGGACATCAAGCTCGGAGATTAAGATGAGACCAAGAGATTTGT 122
304 ACAAACATTTAAGAGAGCGCGTGAATTTCAATTCATCTCCAGTCCATGACGAC 363
123 TTGACTCATTTGAAGAAAGGCAATCAGCGCTTCTCATCTCCAGGACATGATGACAC 182
364 TGGCGGAGATTTAAGAGATTTCCCATTTCTGATGCGCTTGGATTAATCTCTGCT 423
183 TGGCGTGGAGATTTAAGATTTCTGATGCTTATGCGAGCTTGAATCATTAATTTAT 242
424 ATCACTGGGCGTTGAATTAAGTCTTAATCTGAAGAAATTAAGAAATATGCGTTAC 483
243 GTGACTGAGACATTAACACTGCTTCTCATTTGGAACACCAAGAGAGATCCGCGGTAT 302
484 CTTATATCATCAAAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 543
303 CTTATATCATCAAGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 362

OTHER INFORMATION: Clone ID: PAT_MRT4530_7165C.1
US-10-437-963-71159

Query Match 45.4%; Score 1162; DB 8; Length 2355;
Best Local Similarity 72.5%; Pred. No. 7.7e-308;
Matches 1504; Conservative 0; Mismatches 570; Indels 0; Gaps 0;

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QY 213 GCGGATGACGTTCCGAGAGAGAACCCCAACGTAAGTCTTGGCCCAAGTCCGAGTTAA 272
DB 267 GAGAACTAGTTTGTCTTAAGCAATCTCTTAAGTGAACATTTCCAGCTTATCAAGCTTGA 326
QY 273 GGATATTGAGAGATGACCCCAAGAGATTGTGACAAAACATTAAGAGGCGCTGAAGTTT 332
DB 327 GGAGATGAAGCTGTTCAGGGGAAGCTGTATTATCTCTTAAGAGGCAATTCCTCG 386
QY 333 CCATTCAACTCTCCAGTCCCATGACGACACTGGCCGGGAATTATGAGAGTCCCATTT 392
DB 387 TTATTTCTACTTTTCAGACACATGATGACACTGGCTGGGATTAATGTGTCCCATGTT 446
QY 393 TCTGATGCTGGCTGTGTAATTACTCTGTCTATCATCTGGGCGTTGAATACAGTCTTAAC 452
DB 447 CTTATGCGCAGGCTTGATTTATTAACATTATATGAGCGGAGCGCTGAACACTGCTTGTTC 506
QY 453 TGAAGACATAGAAAAGAAATATGCGCTTACCTCTATATCATCAAAAACAAGATGTGG 512
DB 507 ATCTGAACATCAAGAGAGATACGGCGGTATCTCAACATCATCAAGATGAAGTAGAG 566
QY 513 GTGGGTTTGCATATTGAAGTCCAAAGCAACATGTTGGCTGTCTGTGAGTTATTTAC 572
DB 567 ATGGGTTTGCATATTGAAGGCAACAGCACATGTTGGCTCAAGGTTGACATATGTTTC 626
QY 573 TCTGATTTGCTAGGTGAGGGGCTTATGATGACAAAGGAAATGAGAGGCAACGTA 632
DB 627 TTTGAGATTTGCTTGGGGAGGGGCCAGATAGCGGCATGAGCTATGAGAAAGACGAAA 686
QY 633 CTGATTTCTAGGCGCATGCTGTCTACTATATAACGTCATGAGGGAAGATGTGGCTTTC 692
DB 687 ATGAGTTTAAACATGAGGGAGGCACTTATATTAATCATATGAGGCAAGTTTGGCTTTC 746
QY 693 AGTACTTGGAGTGTATGAAATGCTGTGGAATATATCCCTGCGCCCTGAGATATGCTCT 752
DB 747 GGTGTGTGTGTATTTGACTGTGTGCGCAACCAACGTCGCAACCAAAATATGTTGTT 806
QY 753 TCCATACATGCTTCATTTCAATCCAGAAAGATGATGTCATGCGCGGATGTCTATTT 812
DB 807 GCCATATTTCTGCGGATTTCAATCCAGGCGCAATGTGTGTCAATTTGCCGAGTTTATTT 866
QY 813 GCCGATGCTCTATTTATATGCAAGAGGTTTGTGTCCAATCTCACCAACAGATTTATTC 872
DB 867 GCTATGTGTTCATTTATGAAAGAGGTTTGTGGCCCAAGTTACCAAAATTAATTTGA 926
QY 873 TTTGAGAAAAGAGCTTTATACATGACATACATGATATTAATTTGGGATCCGCTCGAA 932
DB 927 ATTATAGAAAGAGAACTCTACGAAGTACCTTACATGATGATTTGGGCAAGGCTCGCA 986
QY 933 TTTGTGTGCAAAAGAGATTTGTACTATCTCAACCACTTGTACAGATTTCTTTGGGC 992
DB 987 TCTATGTGCTAAGAGATCTGTACTATCAATTCATTTGCTGAGAGATTAATTTGGGC 1046
QY 993 ATCTCTACAAAGTTCTTGAAGCTTATCTGATGATTTGGCTGGAAGAAATGAGGGA 1052
DB 1047 CACTCTCCAAAAATTTGTGTAACCAAGCTATGTGTGGCTGGGAACAATTTGAGGGA 1106
QY 1053 AAAAGCTTATTTCTGATTTGAGCATATACATTTACGAAGATGAAGTACTCGATATAT 1112
DB 1107 GAAAGCTTTGACACTGTGATGACAGCATATTCATTAATGATAGAGAACCCCATATAT 1166
QY 1113 TTGATAGGCTCTGTAATTAAGTGTTAATATGCTTGTGTGGGGAAGATCCAAA 1172
DB 1167 TTGATTTGTGTCAGTAACAGGATTAATATGCTTGTGTGAGATTAAGATCCAAA 1226
QY 1173 TTCTGAGGCTTCAAGTTGATCTTCCAGAGATTTATGATTTATGATTTGACAGAGA 1232
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DB 1227 CTCAGAGCATTCCAACTCCACATTCCAAGATGCCAGATTAACCTATGATTCAGAGAGA 1286
QY 1233 TGGCATAAANAATGAGGCTTACAAATGGAATCAACTATTTGGGACATCTCTTTGTGTCCA 1292
DB 1287 TGGCATAAAATGAGGCTTATTAATGGAACCGAGCTGTGGAGCACACTTTCAAGTTTCA 1346
QY 1293 AGCAATTAATTTGACATCTAACCTCAATTGGAAGATTTGTGCAACTATAAGAAAGCTCTAC 1352
DB 1347 AGCTATAGTGTGCTACTGCGCTCAATGGAAGATTTGTGCTCACTTTAACTAGACATGG 1406
QY 1353 CTATATTTAAGAAATTCACAGGTTTGAAGATTTGCTCAGGTGATCTTAATTAATGTTACG 1412
DB 1407 CTACATATAAAGAAACGAGGTTATCGATGACTGCCCTGAGATCTTATGCTAGTGTACCG 1466
QY 1413 TCGATTTCAAAAGTGTGCTTTTCACTGAGATCAATGGAATGSCCAATTTCTGA 1472
DB 1467 CCAATATCTTAAGGTGACATGCGCTTTTCTACTGCTGATCAATGTTGGCCCTATATGAGA 1526
QY 1473 CTGACAGCTGAAGAGCTGAAGCTGTTCTATTAATCTACAAAATTCACACAGAAATAGT 1532
DB 1527 TTGCACTGCAAGAGGACTTAAGCGGCAATTTGCTATCGAAGTTTCTCAGATATTTGT 1586
QY 1533 TGTGACCAATAGACGTGAAGGATTAATGATTTCTGAATATGTCAATCTCTCACTACA 1592
DB 1587 TGGCGAAGCAGTGAAGTTAATAGACTGTATGATTTCTGCAATTTGTTGATGTCAATCAT 1646
QY 1593 GAATGAAGATGTGCTTTTTCACATATGAGCTTAAACGATCTTAATATGTTGGAT 1652
DB 1647 GAATGAATTAATGTGTGATTTTTCACATATGAGCTTCAACAGGCTTATGCTGCTGAGCT 1706
QY 1653 AATCAATCTGCTGAACCTTTTGTGACATGTTATGATTAATCTTATGTAATGATATAC 1712
DB 1707 TATCAATCTGCTGAGACCTTTGGGACATTTGATTTATTCCTTATATGGAATGACAC 1766
QY 1713 ATCAGACGATTCAGCTTTTGGCATTTAGAAATTAATTCCTGGGCAATCCCGAGA 1772
DB 1767 TTCAGCAGCAATTCAGGCTTGAACAGATTTAAAGCTCTTACCTGAGACCGCAAGAG 1826
QY 1773 AGAAATCAACATTTGATTCGATTAAGCACTACCTTCATGAAATAATACAGCTTCGA 1832
DB 1827 TGAATATGACAACTGATTAAGCAAGGCTGCTAGCTTATTAAGGGATTTCAAAAAACGA 1886
QY 1833 TGGATCATGATATGATCTTTGGGAGTTTGTCTTCACTTACGAGTCTTGTGGGCTTAAA 1892
DB 1887 TGGTTCAATGATATGATCTTTGGGCTGTTTGTTTTAACTATAGGCAATGTTTGTGTTAA 1946
QY 1893 AGGTGATTTGCTGTGGAAGAGGTTTCAATTAATGCTCAAGCATCCGTAAGCTGTGA 1952
DB 1947 GGGATTAATGTTGCTGTGTAAGCAATTCAAAAACAGTCCGCAATCAGAAAGCATGTGA 2006
QY 1953 ATTTTGTGCTTCCAGAGGCTTCTTGTGTGCTGGGAGAGAGATTAATCTGTCTGTCA 2012
DB 2007 CTTTGTGTGTCAAAAGAGCTTCTTCTTGTGAGGCTGGGAGAAAGCTTAATTTGTCATCCA 2066
QY 2013 AAAACAAGTATTTCAATCTGGAAGGCAACAGTCTCATGTGTCACACTGGGTGGGC 2072
DB 2067 AGATCAGGTTTATACATCTCGAAGGAGACCACTCATGCGGTGAACACTGTTGGGC 2126
QY 2073 TATGTTGGCTCTCATTTGATGATGCTGAGACAGGCTTAAGAGATTTCCCAACACTGACCGGGC 2132
DB 2127 CATGCTAGGCTTATTCATGATCAGGCGAGGCTGAGAGAGATTCCAATCTTTGCAATCGAGC 2186
QY 2133 AGCTGCACTTTGATTAATTTCCCAATTTGAGAGACGTTGACTTTTCCGAGAGAGAAATAT 2192
DB 2187 AGCGAAGTTTGTATCAACTTAACATTCGAAGATGTGAATTTTCCAGAGAGAGATCAT 2246
QY 2193 GGGAGCTTTCACAAAGATTTGATGATCAATTCAGCGCGGATTCAGAAACATATTTCCCAT 2252
DB 2247 TGAAGTCTTCAACAAAACGTCATGATCACTCTCGAGATTAAGAAACATCTTCCCTAT 2306
QY 2253 TTGGGCGTTGGGAGAAATCCCAATCCCAAGTATTG 2286
DB 2307 TTGGGCGCTTGGGAGATGATCCGTGCGCGGTCTTG 2340
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RESULT 10
 US-10-425-114-24593
 / Sequence 24593, Application US/10425114
 / Publication No. US20040034888A1
 / GENERAL INFORMATION:
 / APPLICANT: Liu, Jindong
 / APPLICANT: Zhou, Yihua
 / APPLICANT: Kovalic, David K.
 / APPLICANT: Screen, Steven E.
 / APPLICANT: Tabaka, Jack E.
 / APPLICANT: Cao, Yongwei
 / TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 / FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 / FILE REFERENCE: 38-21(5313)B
 / CURRENT APPLICATION NUMBER: US/10/425,114
 / CURRENT FILING DATE: 2003-04-28
 / NUMBER OF SEQ ID NOS: 73128
 / SEQ ID NO 24593
 / LENGTH: 2653
 / TYPE: DNA
 / ORGANISM: Zea mays
 / FEATURE:
 / OTHER INFORMATION: Clone ID: LIB3632-042-C4_FLI
 US-10-425-114-24593

Query Match 44.7%; Score 1145.6; DB 8; Length 2653;
 Best Local Similarity 70.3%; Pred. No. 2.7e-303;
 Matches 1578; Conservative 0; Mismatches 639; Indels 29; Gaps 2;

QY 49 GGAGGAATTCATGCTTGGCATTTGAAATCAATCACTTGAAGAGAGAGAGTGTGGAGTTC 108
 DB 175 GGGGGGAGACCCCTGGCTCCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTC 234
 QY 109 GATCTTAAGCTTGAATGCGCGCAAGATCTCTCGAGATTGAGAAAGTCCGCAAAATTT 168
 DB 235 GAGGCC-----TCCGCGAGCCCGAGCCCGCGTCCGCGCGCGCGCGCGCTTC 285
 QY 169 CACGATTAACCGCTTACCCCAAAACAAGCGCTGATCTTATATGGAGTCAAGTTCGCA 228
 DB 286 GCGCGGAG 345
 QY 229 AGAGAGAACCCACAGAGTGTGCTTGGCCCAAGTCCCAAGTGAAGTATTTGAGATG 288
 DB 346 AAGAGAAATCTCTTGAAGTTCAGCTTCCAGCATCAAGTCCGATGAGAGAGAGAGAT 405
 QY 289 ACCCAAGAGATTTGACAAACATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 348
 DB 406 ACCGAG 465
 QY 349 TGCCATGAG 408
 DB 466 GCAATGATGAG 525
 QY 409 GTAATTAATCTGCTTATCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 468
 DB 526 ATCAATTAATCTGCTTATCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 585
 QY 469 GAATATGAT 528
 DB 586 GAGATCGGTGAGATCTTTATTAATCATCAAGATGAGATGAGATGAGATGAGATGAGAT 645
 QY 529 GAAGGTGAT 588
 DB 646 GAGGTGAT 705
 QY 589 GAGGGGCTAATGAT 648
 DB 706 GAGGAGAGAGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 765
 QY 649 GGTGTCTAATTAATCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 708

DB 766 GCGGAGCAATATATTAACATCTGGGAGAGATTTGGCTCTCGGTACTGTGTATTT 825
 QY 709 GAATGTCTGGAATAATCCCTCGCCCTGAGATGAGTCTCTTCAATACATGCTTCA 768
 DB 826 GAATGTCTGGAATAATCCCTCGCCCTGAGATGAGTCTCTTCAATACATGCTTCA 885
 QY 769 TTTCAATCCAGAGAGATGAGTCTGATCAGCCGAGATGCTATTTTGGCCGATGCTTACTTA 828
 DB 886 TTTCAATCCAGAGAGATGAGTCTGATCAGCCGAGATGCTATTTTGGCCGATGCTTACTTA 945
 QY 829 TATGCAAGAGATTTGTTGCTCAATCTCACCACAGATTAATCTTTGAGAGAGAGAGAT 888
 DB 946 TATGCAAGAGATTTGTTGCTCAATCTCACCACAGATTAATCTTTGAGAGAGAGAGAT 1005
 QY 889 TATACAGTACATACATGATTAATGATGAGATGAGTCTCAGATTTTGGAGAGAGAGAT 948
 DB 1006 TTTCAAGAGATTTGTTGCTCAATCTCACCACAGATTAATCTTTGAGAGAGAGAGAT 1065
 QY 949 GATTTGATCTATCCCTCACCACATTTGATGAGATTAATCTTTGAGAGAGAGAGAT 1008
 DB 1066 GATTTGATCTATCCCTCACCACATTTGATGAGATTAATCTTTGAGAGAGAGAGAT 1125
 QY 1009 CTGAGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1068
 DB 1126 GTTGAACAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1185
 QY 1069 GCATTTGAGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1128
 DB 1186 GCATTTGAGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1245
 QY 1129 AATTAAGTCTTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1188
 DB 1246 AATTAAGTCTTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1305
 QY 1189 TTGATCTTCCAGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1248
 DB 1306 CTTCATCTCCAGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1365
 QY 1249 GGTAAATGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1308
 DB 1366 GGTAAATGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1425
 QY 1309 AACCTGATGAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1368
 DB 1426 AACCTGATGAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1485
 QY 1369 CAGTTTGAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1428
 DB 1486 CAGTTTGAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1545
 QY 1429 GCTTGGCTTTTCAATGAGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1488
 DB 1546 GATGAGATTTTCAATGAGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1605
 QY 1489 CTGAAGATTTTCAATGAGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1548
 DB 1606 CTGAAGATTTTCAATGAGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1665
 QY 1549 GTGAAGATTTTCAATGAGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1608
 DB 1666 GTGAAGATTTTCAATGAGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1725
 QY 1609 TTTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1668
 DB 1726 TTTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1785
 QY 1669 ACTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1728
 DB 1786 ACTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1825
 QY 1729 GCTTGGCAATTTTGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1788
 DB 1826 GCTTGGCAATTTTGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1885

Qy	1789	ATCGATAAAGCACA	CTACTCTTCA	TGAAATAA	TACAAGCTT	CAGATGAT	CACTGTGTA	TGCT	1848						
Db	1886	ATCGAACAAGCTG	CTAAATTTCA	TGAGAGCA	TTCCAGAA	ATGACGGT	CTACATGTA	TGGC	1945						
Qy	1849	TCTTGGGGAGTTG	CTCACTTAC	GGAGCTTG	TGTTGGGGTAA	AAAGCTG	ATATGCTG	CT	1908						
Db	1946	TCTTGGGCTGTT	GTGTTTCA	CGTACGG	CACTGGTGT	TGTGAA	GGGACTAA	TTCGCT	2005						
Qy	1909	GGAAAGAGTTT	CAGTAATTTG	CTCAAGCA	TCCGTAA	AGCTTG	ATATTC	TGCTCCAG	1968						
Db	2006	GGTGAACATTT	GAAGAGCA	GTCTCTG	CAATCAGAA	AAAGCATC	CGCTTTCT	GTATCAAAA	2065						
Qy	1969	CAGCTTCTT	GTGTGTG	CTGGGAG	AGATTAT	CTCTCT	GTCAAA	ACAAGGTG	ATTTCA	2028					
Db	2066	GAGCTTCTT	CCGGTGG	CTGGGAG	AAAGCTAT	TATTTAT	TGCTCA	AGACCA	GGTTTAC	2125					
Qy	2029	AATCTGGAAG	GCACAG	GTCTTC	TATGTGT	CAACACT	GGGTGG	CTATTTGG	CTCTCAT	2088					
Db	2126	AATCTCAAA	AGGCAC	CCGAGCT	CAATGCA	CCGAAC	CTGTGTT	GGGCAT	CTCTGG	CTGTAT	2185				
Qy	2089	GATGTGGA	CAGGCTAA	GAGAGATT	CGAAC	CACTGCA	CCGGAG	CAGCTG	CATCTG	ATA	2148				
Db	2186	GATGAGGA	CACAGGCC	CAAGAG	ATCTCC	GCCTTCA	CCAGCA	CAGCAG	GGTTTT	GTATA	2245				
Qy	2149	AATTC	CCAA	TGTGAG	AGCGT	GACTTTT	CCGAC	AGCA	GAATAAT	TATGGAG	GTCTTCA	CAAG	2208		
Db	2246	AAC	TTGC	AGTCA	GAGAG	ACGGA	AAATTTCC	CA	GCAAG	AGATCAT	TATGAG	GTCTTCA	CAAG	2305	
Qy	2209	AATTC	GATGAT	CACAT	ACGCG	CAATAC	AGAAA	CATATTTCC	CA	ATTG	GGGCTT	GGGAGA	2268		
Db	2306	AAT	GCATGAT	CA	GTATCT	CC	CA	AGTAC	AGAA	CA	CTCCG	ATCTGG	GCCTT	GGGAG	2365
Qy	2269	TACCA	ATCCCA	AGATTG	SCAAT	CTCG	2294								
Db	2366	TAC	CGATCC	AGATCT	CTGG	AGCTGG	2391								

```

RESULT 11
US-10-221-074-3
; Sequence 3, Application US/10221074
; Publication No. US20030208791A1
; GENERAL INFORMATION:
; APPLICANT: Bryan, Gregory T.
; APPLICANT: Hwang, Der-Chyan
; APPLICANT: Maxwell, Carl A.
; APPLICANT: McGonigle, Brian
; APPLICANT: Potter, Susan M.
; TITLE OF INVENTION: ENZYMES INVOLVED IN TRITERPENE SYNTHESIS
; FILE REFERENCE: BBI38 PCT
; CURRENT APPLICATION NUMBER: US/10/221,074
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/188,054
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 2478
; TYPE: DNA
; ORGANISM: Glycine max
US-10-221-074-3

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Query Match	36.9%;	Score 944.2;	DB 7;	Length 2478;
Best Local Similarity	64.7%;	Pred. No. 6.4e-248;		
Matches 1469;	Conservative	0;	Mismatches 788;	Indels 12;
				Gaps 4;

Qy	23	GAATGTGGAAGCTCAAGTTTCGCCAAGAGGGA	---	ATTCATGCGTTTGGACATTGAACA	79
Dy	32	GGAATGTGGAAGCTGAAGATACAGATGGAAGAAATGATCCATACATATTCACCAACAAACA			91
Qy	80	ATCAGCTTGAAGAACAAGGTGTGGAGTTTCGATCTCTTAAGCTTGGATCGCGCAAGATCTCC			139
Dy	92	ATTTCGTTGGAGGCGACATGGGAGTTTGAATCTCGAAGACAGGCGAGTCCAGAGGAAACGGG			151

QY	140	TCGAGATTGAGAAAGCTCCGCAAGATTTTCACGTAATCCGCTTTAACCAACAACAGACGC	199
Db	152	CCGAGGTGGAAGCAGCTGTGCAGCATTTCTACCAACACCGCTTACAAAGGTCAAGCCCTGCG	211
QY	200	CTGATCTACTATATGGGAGATGACGTTCCGCAAGAGAACCCCAACAGTGAAGCTTGCCCA	259
Db	212	CTGACCTCTCTTTGGCGTTTCAAGTTCTCAAGAGAAATTAATCTTCAACACAAACAATTCCTC	271
QY	260	AAGTCGAGTTAAAGATATTGAGATGTGACCCAAAGATTTGTGACAAAACATTTAAGAA	319
Db	272	GTGTGACTATATGAAGATGAGAGGAAATCATATACAAAAGATGACAAAGCCCGTCAGAA	331
QY	320	GGGCCGCTAAGTTTCCATTCAACTCTCCAGTGCATGACGACACTGGCCGGAGATTATG	379
Db	332	GGGGGCGCACACCACTTCGCGCACCTGCAGACCTCTGATGGCCATTGGCGCTCTCAAAATTG	391
QY	380	GAGGTCGATGTTCTGATGTCGCGCTTGGAATTAATCTGTGTATCACTGAGGGGCTTGA	439
Db	392	CAGGTCCTCTCTTCTTCTCTCTCCCTGGTTTTTGTATATATTTACAGAAATCTTG	451
QY	440	ATACAGTCTTAATCGAAGACATAGAAAGAAATATGCGCTTACCTCTATATCATCTCAA	499
Db	452	AATCAGTATTTCCAGAAAGACATCGCAAGAAATTTCTTGTTACACATTTATCAACAGA	511
QY	500	ACAAGGATGTGGGTGGGGTTGCATATTTGAAGTCCAGACACATGTTGGCTCTGTCT	559
Db	512	ATGAAGAAGGAGATGGGGACTACACATAGAGGCTCATAGACATATGTTTGTACTGAC	571
QY	560	TGAGTTATATATCTGTGATTTGCTAGGTGAGGGCCCTAATGATGAGCAAG---GGGAAA	616
Db	572	TGAATATATATATGCAATGCGAATGCTTGGAGAGAGCCTAATGAGGTCATACAAATGCTT	631
QY	617	TGGAGAAAGCAGCTGACATTTCTGAAGGCACTGGTGGTCTACTTATATTAACGTATCGG	676
Db	632	GTGCTAGAGCAAGAAAGATTTGAGATCATGTGGTGTATACATATTAATCTTCAATGAG	691
QY	677	GGAAGATGTGCTTCACTTCTGAGTGTGAATGTCTGGAATATATCCCTGCCCC	736
Db	692	GAAAAAATTGGCTTTCGATCTACGCTGATATTGATTTGGTGGGGAAGCAACCAATGCCCC	751
QY	737	CTGAGATATGGCTCCTTCATATACATGCTTCCATTTCAATCCAGAAAGATGTGGTCACT	796
Db	752	CAGAGTTTGGATCCTTCCATCTTTCTTCTTAAATGACATCCAGTAAAGTGTGGTACT	811
QY	797	GCCGAGTGTCTAATTTGCCGATGTCTCACTATATATGCGAAGAGTTTGGTCCAACT	856
Db	812	GTGATTTGTATACATGTCTATATGCTTATATATATGGAAGAGTTTGTGGTCCAACTA	871
QY	857	CACCAACAGTATTAATCTTTGAGAAAGAGCTTTATATACAGTACCAATACCAGATATATAT	916
Db	872	CACCACTCATCTTACAAATTAAGAGAAAGTTGTTTACTCAACCTTATGAAAAAGTTAAT	931
QY	917	GGGATCAGGCTGCGAATTTGTGTCAAGAGAAATTTGTACTATCTTCAACCACTTATGAC	976
Db	932	GGAAGAAAGCCGCTGACCAATGTCCAAAGAAAGATCTTATCTATCCCATCTTGTATAC	991
QY	977	AGGATATCTTTGGGCACTCTACACAAAGTCCCTTGAAGCTATCTGATGATTTGGCCTG	1036
Db	992	AAGACTATATATGGGATATGTTTATATACATTTCACTGAAACCGCTACTTAACTGTGGCCTT	1051
QY	1037	GAAGAAAGATG---AGGGAAAGGCTATATTTCTGCAATTTGGAGCATATACATTACGAAAG	1093
Db	1052	TCACAAAGTATTAAGAGAAAGGCCCTTCAAGTACATATGAAACATATTTCAATTATGAAAG	1111
QY	1094	ATGGAATATCTCGATATATTTTGCAATAGGCTCTGTAAATTAAGTGTAAATATGCTTGGCT	1153
Db	1112	ATGAGACTATGCGATACATATACATTTGGTGTGTGAAAAGGTTTATATATATGCTGGCTT	1171
QY	1154	GTTGGGTGGAAGATCCAAATTTCTGAGGCTTCAAAGTTGCATCTTCCAGAGATTATATGTT	1213
Db	1172	GTTGGGTGGAAGATCCAAACGGAATGCTTTCAGAAAGCATCTTGCAGAGGCTCCAGATTT	1231

1214 ATCTATGATTCGAGAAATGCGAATGCAAGGCGTCAATGAGTCACTATGGG 1273
1232 ACTTATGGGTTTCTGAAAGATGAAATGACATGCAAGTT---TTGGTGGCCAAAGATGGG 1288
1274 ACACGCTTTTGGCTGCGCAAGCAATTAATGCACTTAACCTCAATGGAATTTGGTCCAA 1333
1289 ATGCTGGCTTGTCTGTTCAAGCTTTGCTTCCACTTACATTAATTTGAAGAAATTTGGTCTCA 1348
1334 CTATAGAAAGAGCTCAATCTATATTAAGAAATCAAGGTTTGAAGATTTGTCAGGTG 1393
1349 CGTTTGCAAAAGACATGATTTTCACTAAGAGCTCAGGTGAAGATTAATCTTTTGGAG 1408
1394 ATCTTAATTAATGTAACCTGCACTTCAAAAGGTGCTTGGCTTTTCACTGAGATC 1453
1409 ATTTTAAAGATGATCGTCAATTTCTTAAAGGGCTTGGACATTTCTGATCAAGACC 1468
1454 ATGATGCGCAATTTCTGCTGCAAGCTGGAAGAGCTGAAGCTGTATTAATCAATCA 1513
1469 ATGATGCGAAGTTTCTGATGCACTGCAAGAGTTTAAAGTTGTTCTTACTTATCA 1528
1514 AAATGACACCAAAATAGTTGGTGAAGCAATAGACGTGAAGCGATTAATGATTCGTAA 1573
1529 TGTGCGACCAAGATTTGGGAGAAAGATGGAACCTGAAGATTAATGATTCAGTCA 1588
1574 ATGTCAATTCCTCACTACAGAAATGAAGATGGTGGTTTGCACATATGAGCTTAAACAT 1633
1589 ATGCTGTTGTTGCTTCAAGATTAAGTGGTTTACAGCATGGAGCCTGCGAGAG 1648
1634 CTATTAATTTGGTGGATTAATCAATCCCTGCTGAACCTTTGGTGCATCGTATTAATG 1693
1649 CTCAGAGAGTTAGTGAATTAATCAATCCAGAAATTTTGGGAGCATGTAATGTAAC 1708
1694 ATCTTAATGGAATGATATGATCAGCAGCATTCAGCTTTGGCATTAATTAAGAAATTA 1753
1709 ATGAATATTTGATGCTCACTGATCTGCAATCCAGCTTATGTTTGTTCAGAAACAT 1768
1754 ATCTGGGCGATCGCCGAGAAATTAACAATTTGATGATTAAGCAATGACCTTCACTT 1813
1769 ATCCAGGACATAGAGAAAGATAGAAATTTCAATTAACAATGACATTCGATTCCTTG 1828
1814 AAAAATTAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1873
1829 AAGATTAACAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1888
1874 GGTCTGTTGGGTTAAAGATCTGATGCTGCTGGAAGAGATTCAGTAATTTGCTCAA 1933
1889 GCTTGTGTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1948
1934 GCATCCGTAAGCTTGTGAATTTCTGCTGTCAAGCAGCTTCTTGTGCTGGGAG 1993
1949 CCAATTCGCAAGAGCGTTAAATTTCTAATTAACAACAAGAGAGAGCGGTGATGGGAG 2008
1994 AGAGTTATCTGCTCTGCAAAACAAGGTGATTAATTAATTCGGAAGGCAAGGTCTCATG 2053
2009 AGAGTTATCTTCAAGCCCAAAAGATATATGATTAATTAATTAATTAATTAATTAATG 2068
2054 TGGTCAACACTGGGTGGGCTATGTTGGCTCTCAATGATGCTGAAGGCTTAAGAGAT 2113
2069 TTGTACATACAGATGGGCTTATGAGGCTTAATTAATTAATTAATTAATTAATTAATTA 2128
2114 CGCAACCACTGCAACCGGCGAGCTGATTAATTAATTAATTAATTAATTAATTAATTAAT 2173
2129 CCAATGCTCTTCAACCGGTGCAAAAGTTGCTCAATTAATTAATTAATTAATTAATTAAT 2188
2174 TTTCGAGCAGCAAAATTAATGAGGTCTTCAACAAGATTTGATGATCACTAGCCGAT 2233
2189 GGGCCCAACAGAAATCAAGGATATTAATTAATTAATTAATTAATTAATTAATTAATTA 2248
2234 ACAGAAACATATTCCTCAATTTGGGCGTTGGAGAAATCAATCCCAAGT 2282
2249 ACAGAGATATTTATCAATGTTGGCTTACGTGAATTAATCAAGCGGAT 2297

RESULT 12
US-10-427-570A-4
; Sequence 4, Application US/10427570A
; Publication No. US20040010818A1
; GENERAL INFORMATION:
; APPLICANT: McGonigle, Brian
; APPLICANT: Maxwell, Carl A.
; APPLICANT: Hession, Aileen O.
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH A SUPPRESSED TRITERPENE LEVEL
; FILE REFERENCE: B1523 US NA
; CURRENT APPLICATION NUMBER: US/10/427,570A
; CURRENT FILING DATE: 2003-05-01
; PRIOR APPLICATION NUMBER: 60/379,361
; PRIOR FILING DATE: 2002-05-09
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 2478
; TYPE: DNA
; ORGANISM: Glycine max
US-10-427-570A-4
Query Match 36.9%; Score 944.2; DB 7; Length 2478;
Best Local Similarity 64.7%; Pred. No. 6.4e-248;
Matches 1469; Conservative 0; Mismatches 788; Indels 12; Gaps 4;
23 GAATGTGAAGCTCAAGTTCCCGAAGAGGGA--ATCCATGCTTGGACATTTGAACA 79
32 GGATGTGAGGCTGAAGATGAGATGAGAGGAATGATCAATATTCATTAATGACACAAACA 91
80 ATCACTTGAAGAGAGGTTGGGAGTTGATCTCAAGTTGATGATGATGATGATGATGATGAT 139
92 ATTTGTTGGGAGGAGACATGAGGATTTGATCTGGAAGAGGAGCTGCAAGAGAAAGG 151
140 TCGAGATTGAGAAAGCTGCGCAGAAATTTCAAGATACCGCTTTACCAACAACAAGCG 199
152 CCCAGTTGAAGACAGCTGTCAGCATTTCTACCAACAACCGCTTCAAGGTCAAGCCCTGG 211
200 CTGATCTAATTAATGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 259
212 CTGACCTCTTGGGTTTCAAGTTCTCAGAGAAATTAATTAATTAATTAATTAATTAATTA 271
260 AAGTGGAGTTAAGATATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 319
272 GTGTGCTATTAAGAAATGAGATGAGAAATTAATTAATTAATTAATTAATTAATTAATTA 331
320 GGGCGGTAAGTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 379
332 GGGGCGCAACAACCTTGGGCACTGCAAGCTTGAATGATGATGATGATGATGATGATGATG 391
380 GAGTCCCATGTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 439
392 CAGGTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 451
440 ATACATCTTAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAA 499
452 AATCAATATTTCCAGAAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAG 511
500 ACAAGATGTTGGGTTGGGTTGGATTAATTAAGATTAAGATTAAGATTAAGATTAAGAT 559
512 ATGAAGACGAGATGGGATGAGATTAATTAAGATTAAGATTAAGATTAAGATTAAGATTA 571
560 TGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 616
572 TGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 631
617 TGAAGAGGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 676
632 GTGCTAGACCAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 691
677 GGAAGATGAGGCTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 736
692 GAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 751

200 CTGATCTAATTATGCGGATGCACTTCCGAGAGAACCCAAACAGTGAAGCTTCCCA 259
 212 CTGACCTCTTGGCGGTTTTAGGTTCTCAGAGAAATTAATCTTCAACAAATCTTCC 271
 260 AAGTGGAGTTAAGATATGAGGATGAGCCCAAGAGATTTGTGCAAAAACATTAAAGA 319
 272 GTGTACTATAGAAATGAGAGAAATCACTACCAAAAAGTCAACAGCCGCTCAGAA 331
 320 GGGCGGTAACTTCCATTCACCTCTCAGTCCATGACGACATGCGCGGAGATTATG 379
 332 GGGGGCACACCACTTGGGSCATGACAGCTCTGATGGCCATTTGGCTGCAAAATG 391
 380 GAGGTCCCATGTTTCTGATGCTGCTGGTGGTAATTACTGTCTATCACTGGGCGTTGA 439
 392 CAGGTCCTCTCTTCTTCTTCCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 451
 440 ATACAGCTTAACTGAGAAACATAGAAAGAAATATGCGTTACCTTATATCAATCAA 499
 452 AATCAGTATTTCCAGAAACATCGCAAGAAATCTTGTACACATATATCAACAGA 511
 500 ACAAGGATGAGTGGGTTGGCATATTTGAAGTCCAGACACATGTTGGCTGTCT 559
 512 ATGAAAGCAGAGATGAGGACATACATAGAGGTCATAGCATATTTTGTACTGAC 571
 560 TGAATTAATTAATCTGAGATTGCTAGTGAAGGCTTAATGATGACAG--GGGAAA 616
 572 TBACTATATATGACATGCGAATGCTTGAAGAGACCTAATGAGGTCATGACAAATGCTT 631
 617 TGGAGAGGCACTGATGATCTTGAAGGATGAGTGGTGTCTATATATAGCTCATGGG 676
 632 GTGCTAGAGCAAGAAAGTGAATTCAGATCATGGTGGTGAACACATTAATCTTCAATGG 691
 677 GGAAGATGAGGCTTCACTGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 736
 692 GAAAACTTGGCTTGGATCTGAGTGTGATGATGATGATGATGATGATGATGATGATG 751
 737 CTGATATATGAGCTCTTCCATACATGCTTCCATTCATCCAGAGAGATGAGTGTCTACT 796
 752 CAGAGTTTGGATCTTCCATCTTCTTCTATGATCAGGATGATGATGATGATGATGATG 811
 797 GCCGATGCTCTATTTGGGATGCTCTCTATATATGCAAGAGATTTTGTGCTCAATCT 856
 812 GTCTGATGATATCACTGCTATGCTTCTTATATATGGAAGAGTGTGGGCTCAATCA 871
 857 CACCAACAGATATCTTTGAGAAAAGGCTTATACAGTACCATCACTATATAGATT 916
 872 CACCACTCATCTTCAATTAAGAAAGAGTGTGTTACTCAACTTATGAAAAAGTTAAT 931
 917 GGGATCAGGCTCGCAATTTGTGTGCAAGAGAGATTTGATCTATCTCCACCACTTGTAC 976
 932 GGAAGAAAGCGCTCAACAATGCAAGAGAGATCTTATCTATCCCACTTGTATAC 991
 977 AGGATATCTTTGGGATCTCTACACAAGTCTTGAAGCTTATCTGATGATGATGATGATG 1036
 992 AAGACCTAATATGAGGATGATTTATATATCTGAAACGCTATCTTATCTGTTGACCTT 1051
 1037 GAAAAAGATTG--AGGAAAAGGCTATATTTCTGATTTGAGCATATATCAATTAAGAG 1093
 1052 TCACACAGTTGATTAAGAAAAGCGCTTCAAGTAACTATGAAACATATCTATTAAGAG 1111
 1094 ATGAGATATCTCGATATATTTGATAGTCTCTGTAATAGATGATTAATATGCTTGTCT 1153
 1112 ATGAGCTATGCTATATATACATTTGTTGTGTGGAAGAGTTTATATGATCTGCTT 1171
 1154 GTTGGGTGAAGATCCAAATTTGAGGCTTCAAGTGTGATCTTCCAGATTTATAGATT 1213
 1172 GTTGGGTGAAGATCCAAACGAGATGCTTTCAGAAAGCATCTTTCAGAAAGGCTCCAGATT 1231
 1214 ATGATGAGTTGAGAGATGAGCATGAAAATGAGGCTCAATGAGATGATCAATAGG 1273
 1232 ACTTATGAGGTTTCTGAAAGATGAGATGACATGCAAGATT--TTGGTACCAAGATGGG 1288
 1274 ACACTGCTTTTGTGTCCAAAGCAATTAATGATCTTCACTCAATGAAATTTGGTCCAA 1333

1289 ATGCTGCGTGTGCTGCTTCAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1348
 1334 CTATAGAAAAGCTCATACCTATATTAAGAAATCAAGGTTTATGAGATGTTCCAGGTG 1393
 1349 CGTTTGCAAAAAGCATATTTCAATCAAGAGATCTCAGGTGAGAGATTAATCTTTTGGAG 1408
 1394 ATCTTAATTAATGATCCTGATCAATTTCAAAAAGTGTGGCTTTTCAACCTGAGATC 1453
 1409 ATTTTAAAAGTATGATGATGATATTTCTTAAAGGCTTGGACATTTCTGATCAAGACC 1468
 1454 ATGATGSCCAATTTCTGATCTGACAGCTGAGAGCTGAAAGCTGTTCTATTAATCA 1513
 1469 ATGATGSCCAATTTCTGATCTGACAGAGAGTTTAAAGTGTGCTTACTTATCA 1528
 1514 AATATGACCAAGAAATAGTGTGAGCAATAGACGATGATTAATGATTTCTGTA 1573
 1529 TGTGTCACCAAGATTTGTGGAGAAAGATGAACTGAAAGATTAATGATTCAGTCA 1588
 1574 ATGTCAATTTCTGATCAAGATGAAAGTGTGTTTGGCAACATAGAGCTTAAAGAT 1633
 1589 ATGTCTGTGTGCTGCTGATGATTAAGAAAGGTTTGAAGCATGAGGAGCTGCAAGAG 1648
 1634 CTTAATTTGTTGGATTAATCAATCCGTGAAACTTTTGGTGAACATCGTTATTTGAT 1693
 1649 CTCAAGAGTTGATTAATTAATCAATCCAGAAATTTTTCGACATTTGATTTGAAC 1708
 1694 ATCTTATGAGATATGATCATCAGCAGATTTCAAGCTTTGGCATCAATTTAGAAATAT 1753
 1709 ATGAATATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1768
 1754 ATCTGGGATGCGGAGAAATTAACAATTTGATGATTAATTAATTAATTAATTAATTA 1813
 1769 ATCCAGGATCATGAGAAAGATGAAATTTCAATCAATCAATCAATCAATCAATCAAT 1828
 1814 AAAAAATCAAGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1873
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 1889 GCTCTGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1948
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 2009 AAGATTAATTTCAAGCCCAAAAAAGATTAATGATGATGATGATGATGATGATGATG 2068
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 2069 TGTGATATACAGATGAGGCTCTTATGAGCTAATTCATGCTGAGCAGGAGATGAGACC 2128
 2114 CGCAACACTGACAGGAGGCTGATCTTATTAATTTCCCAATTTGAGAGAGGTTGACT 2173
 2129 CCATGCTCTTCAAGCGTGTGCAAAAGTTGCTATTAATTTCAAGTTGAGAGGAGGAT 2188
 2174 TTCCGAGAGAGAAATTAAGGAGCTTCAACAAGATTTGCAATGATCAATGACGCGCAT 2233
 2189 GGGCCCAACAGAAATCAAGGAGATTAATGAAAAATTTGCAATGATGATGATGATGAT 2248
 2234 ACAGAAACATATTTCCCAATTTGGGAGGTTGGAGAAATACCAATCCCAAGT 2282
 2249 ACAGAGATTTTATCCAAATGTGGGCTTATGATGATGATGATGATGATGATGATGAT 2297

RESULT 14
 US-10-424-599-35539
 ; Sequence 35539, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:

Qy	18174	GTCGTTGGTTGGGGTAAAGAGCTCGATGCTGCTGCGAAGAGGTTTCAGTAATTCGTCAA	19333
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Qy	1934	GCATCCGTAAGCTTGATGAAATTTCTGCTGTCCAGCAGCTTCCTTCTGTGTGCTGGGGAG	19933
Db	1955	CCATTCGAAAGCCGTTAAATTTCTACTTACACACAAAGAGAGAGCGGTGATGGGAG	20144
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Db	2015	AGAGTTATCTTTCAAGGCCAATAAAGATATATGATCTCTGAAAGAGCCGATCAATG	20744
Qy	2054	TGCTCAACACTGGGTGGGCTATGTTGGCTCTCATTTAGTGTGACACGGCTTAAGAGATT	21133
Db	2075	TTGTATCATACAGCAATGGGCTCTTAATGGGCTTAATTCATGCTGGACACGGCGATTAAGACC	21344
Qy	2114	CGCAACCACTGCAACGGGGAGCTGCATTCCTGATTAATTTCCCAATTTGGAGACGGTGACT	21733
Db	2135	CCATGCTCTTTCACCGTGTGCTGAAGTTGCTCATTAATTTCTAGTTGGAAAGGGTGATT	21944
Qy	2174	TYCCGACACAGGAATTAATGGGAGTCTTTCACACMAAGATTCAGATCAATACGCCGAT	22333
Db	2195	GGCCCAACAGGAATTCACGGGAGTATCATGAAAAATTCAGATGTTCATATCAATGT	22544
Qy	2234	ACAGAAACATATTCCTCCATTTGGGCGTTGGAGAAATACCAATCCCAAT	2282
Db	2255	ACAGAGATATTTATCCAAATGTGGGCTCTAGCTGAATATTCGAAGGGGGT	2303

RESULT 15
US-10-607-726-3

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1 / Sequence 3, Application US/10607726
2 / Publication NO. US20040121439A1
3 /
4 / GENERAL INFORMATION:
5 / APPLICANT: Falco, S. Carl
6 / APPLICANT: Farnoud, Omolayo O.
7 / APPLICANT: Hitz, William D.
8 / APPLICANT: Kinney, Anthony J.
9 / APPLICANT: Rafalski, Antoni
10 / APPLICANT: McGonigle, Brian
11 / APPLICANT: Lohman, Karin
12 /
13 / TITLE OF INVENTION: Enzymes Involved In Squalene Metabolism
14 / FILE REFERENCE: B0113 US NA
15 /
16 / CURRENT APPLICATION NUMBER: US/10/607,726
17 / CURRENT FILING DATE: 2003-06-27
18 / PRIOR APPLICATION NUMBER: 03/09/419, 679
19 / PRIOR FILING DATE: 1999-10-15
20 / PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/105,405
21 / PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-23
22 /
23 / NUMBER OF SEQ ID NOS: 16
24 /
25 / SOFTWARE: Microsoft Office 97
26 /
27 / SEQ ID NO 3
28 /
29 / LENGTH: 1882
30 /
31 / TYPE: DNA
32 /
33 / ORGANISM: Oryza sativa
34 /
35 / US-10-607-726-3

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	Query Match	36.9%	Score 944	DB 8	Length 1882
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Db	74 GTTGTGGCATATTTCTCCGATTCATCAGGGCGAATGTGTGTATTTGTCGGATG				133
Qy	807 CTAATTGGCCGATGCTCTACTTATATGCAAGAGTTTGTGTCCAAATCTACCAACGT				866
Db	134 TTAATTTGCTATGTGTATCAATTATGGAAGAGTTTGTGGCCCGCATGACCAATAT				193

QY	867	TTTATCTTTGAGAAAAGCCTTTATACAGTACCAATACAGATATATAGTTGGATTCAGGC	926
Db	194	ATTGGAATTAAAGAAAGAACTTACGAAGTACCTTACATGAAAGTTGTTGGCAAGGC	253
QY	927	TCGCAATTGTGTCGCAAGGAAGATTTGTACTATCTCCACCCACTGTGACAGATATTTCT	986
Db	254	TCGCAATCTATGTGCTAAGGAAGATCTGTACTATCCACATCCACTTGGTGACAGATGTATT	313
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Db	314	ATGGGCCACTCTCCACAAATTTGTTGAACGACGATATGTTGGCTGGCCCTGGGAACAAATT	373
QY	1047	GAGGGAAGAGCCTATTTATTTTGTGATGGAGCATATACATTACGAAGATGGAATATCTCG	1106
Db	374	GAGGAGAGAAACCTTTGGACACTGTGCACAGACATATTCATTATAGATGGAACACCCG	433
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Db	554	AGAAAGTGCATGAAAATGACGAGGCTTAAATGGAAGCCAGCTGTGGGCAACAGCTTTTCCAC	613
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Db	1154	AAGCATGTGTCATGTGTAATGTCTTTGGGCTGTGTTTATCTATATGCAACATGTGTTGG	1213
QY	1887	GGTAAAGAGTCTGATTTGCTGCTGGAAGAGTTTCAGTAATTTGCTCAACATCCGTAAGC	1946
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Qy      2187 AATTAATGGAGTCTTCAACAAGAATTGCATGATCAGATACGCCGATACAGAAACATATT 2246
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Job time : 2709 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2006, 21:34:53 ; Search time 445 Seconds
(without alignments)
10764.132 Million cell updates/sec

Title: US-09-419-679-5

Perfect score: 2560
Sequence: 1 ttggcctcttgcagcaaaa.....agatataaaaaaaaaa 2560

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1183.6	46.2	2558	US-09-419-679-1	Sequence 1, Appli
3	944	36.9	1882	US-09-419-679-3	Sequence 3, Appli
4	563.8	22.0	1300	US-09-419-679-7	Sequence 7, Appli
5	304.8	11.9	4346	US-09-919-039-112	Sequence 112, App
6	280.2	10.9	4239	US-09-815-048-1	Sequence 1, Appli
7	211	8.2	2196	US-09-614-221A-308	Sequence 308, App
8	74.4	2.9	747	US-09-248-796A-3811	Sequence 3811, Ap
9	72.2	2.8	652	US-09-533-559-4882	Sequence 4882, Ap
10	70.4	2.8	539	US-08-998-416-229	Sequence 229, App
11	58.2	2.3	173	US-09-313-294A-804	Sequence 804, App
12	47.2	1.8	3600	US-10-104-047-1011	Sequence 1011, Ap
13	46	1.8	1141	US-09-806-708B-22	Sequence 22, Appli
14	44	1.7	1664876	US-08-916-421B-1	Sequence 1, Appli
15	44	1.7	1664876	US-09-692-570-1	Sequence 1, Appli
16	43.6	1.7	403	US-08-956-171E-767	Sequence 767, App
17	43.6	1.7	403	US-08-781-986A-767	Sequence 767, App
18	43	1.7	1141	US-09-806-708B-22	Sequence 22, Appli
19	42.8	1.7	63183	US-09-949-016-13047	Sequence 13047, A
20	42.8	1.7	63183	US-09-949-016-13048	Sequence 13048, A
21	42.6	1.7	3091	US-09-949-016-3440	Sequence 3440, Ap
22	42.6	1.7	3217	US-09-949-016-2400	Sequence 2400, Ap
23	42.6	1.7	3236	US-09-949-016-2399	Sequence 2399, Ap

C 24	42.6	1.7	3463	3	US-09-949-016-1417	Sequence 1417, Ap
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C 26	42.6	1.7	4287	2	US-08-306-631B-53	Sequence 53, Appli
C 27	42.6	1.7	62474	3	US-09-949-016-15182	Sequence 15182, A
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C 29	42.6	1.7	121234	3	US-09-949-016-14142	Sequence 14142, A
C 30	42.6	1.7	140315	3	US-09-949-016-14141	Sequence 14141, A
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C 32	41.2	1.6	7218	2	US-08-232-463-14	Sequence 14, Appli
C 33	40.4	1.6	255	3	US-09-248-796A-3810	Sequence 3810, Ap
C 34	40.4	1.6	1599	3	US-09-277-565-16	Sequence 16, Appli
C 35	40.4	1.6	1830121	3	US-09-557-884-1	Sequence 1, Appli
C 36	40.4	1.6	1830121	3	US-09-643-990A-1	Sequence 1, Appli
C 37	40.4	1.6	1830121	3	US-10-158-865-1	Sequence 1, Appli
C 38	40	1.6	5319	2	US-08-861-464-7	Sequence 7, Appli
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C 40	40	1.6	5319	3	US-09-323-433A-7	Sequence 7, Appli
C 41	40	1.6	5319	3	US-09-826-752-7	Sequence 7, Appli
C 42	40	1.6	640681	3	US-09-790-988-1	Sequence 1, Appli
C 43	39.8	1.6	3081	3	US-09-319-989-9	Sequence 9, Appli
C 44	39.8	1.6	3360	3	US-09-319-989-8	Sequence 8, Appli
C 45	39.8	1.6	42450	3	US-09-815-048-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1						
US-09-419-679-5						
Sequence 5, Application US/09419679						
Patent No. 6630617						
GENERAL INFORMATION:						
APPLICANT: Falco, S. Carl						
APPLICANT: Famodu, Omolayo O.						
APPLICANT: Hitz, William D.						
APPLICANT: Kinney, Anthony J.						
APPLICANT: Rafalski, Antoni						
APPLICANT: McGonigle, Brian						
APPLICANT: Lohman, Karin						
TITLE OF INVENTION: Enzymes Involved in Squalene Metabolism						
FILE REFERENCE: B8113 US NA						
CURRENT APPLICATION NUMBER: US/09/419,679						
CURRENT FILING DATE: 1999-10-15						
EARLIER APPLICATION NUMBER: 60/105,405						
EARLIER FILING DATE: 1998-10-23						
NUMBER OF SEQ ID NOS: 16						
SOFTWARE: Microsoft Office 97						
SEQ ID NO 5						
LENGTH: 2560						
TYPE: DNA						
ORGANISM: Glycine max						
US-09-419-679-5						
Query Match						
Best Local Similarity 100.0%, Pred. No. 0;						
Matches 2560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
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Qy 1921 AGTAATTTGCTCAACGATCCGTAAGGCTTGGAATTTGCTGCTGCCAAGCGCTCTTCT 1980
Db 1921 AGTAATTTGCTCAACGATCCGTAAGGCTTGGAATTTGCTGCTGCCAAGCGCTCTTCT 1980
Qy 1981 GGTTGGCTGGGAGAGATTAATCTGCTCTGTCAAAACAAAGGTGTAATCAATCTGGAAGGC 2040
Db 1981 GGTTGGCTGGGAGAGATTAATCTGCTCTGTCAAAACAAAGGTGTAATCAATCTGGAAGGC 2040
Qy 2041 AACGTTCTCATGTGTCAACATGSGGTGGCTATGTTGGCTCTCATTTGATGCTGACAG 2100
Db 2041 AACGTTCTCATGTGTCAACATGSGGTGGCTATGTTGGCTCTCATTTGATGCTGACAG 2100
Qy 2101 GCTTAAGAGATTTGCAACCACTGCAACGGGCAAGCTGCATATCTGATTAATTCACCAATG 2160
Db 2101 GCTTAAGAGATTTGCAACCACTGCAACGGGCAAGCTGCATATCTGATTAATTCACCAATG 2160
Qy 2161 GAGGACGATGACTTTCCGACAGAGAAATATGGAATGGAATCTTCAACAGAAATTCATGATC 2220
Db 2161 GAGGACGATGACTTTCCGACAGAGAAATATGGAATGGAATCTTCAACAGAAATTCATGATC 2220
Qy 2221 ACATAGCCGCGATACAGAAACATATTCCTCAATTTGGGCTTTGGAGAAATACCAATCCCA 2280
Db 2221 ACATAGCCGCGATACAGAAACATATTCCTCAATTTGGGCTTTGGAGAAATACCAATCCCA 2280
Qy 2281 GTATTTGAATCTCGTTAATGAGGCTTAATGAGGCTGATGCTCAATTAATTTGCAACCTGT 2340
Db 2281 GTATTTGAATCTCGTTAATGAGGCTTAATGAGGCTGATGCTCAATTAATTTGCAACCTGT 2340
Qy 2341 GGAAGTAAAGAAATATAATAATACTAATTTTCTTTTATTTCCATGGCTCTCTTAA 2400
Db 2341 GGAAGTAAAGAAATATAATAATACTAATTTTCTTTTATTTCCATGGCTCTCTTAA 2400
Qy 2401 AATGTTTGTGACTAATGAGTTTATGATGCTAGCTTAAAAAAAACCAACACGTGAGAT 2460

Db 2401 AATGTTTGACTAATGAGTTAAGTACGCTAAAGAAAAAGCAACAGTGGAGAT 2460
Qy 2461 GCGTAAAGTTTTTTCTATTACTCATAGACGCTCTCTTTCCTTCCAGCAAGGAA 2520
Db 2461 GCGTAAAGTTTTTTCTATTACTCATAGACGCTCTCTTTCCTTCCAGCAAGGAA 2520
Qy 2521 TTAATATATATACATAATAGAGATATATAAAAAAAAAAAAAA 2560
Db 2521 TTAATATATATACATAATAGAGATATATAAAAAAAAAAAAAA 2560

RESULT 2

US-09-419-679-1

Sequence 1, Application US/09419679

Patent No. 6630617

GENERAL INFORMATION:

APPLICANT: Falco, S. Carl

APPLICANT: Ramodu, Omolayo O.

APPLICANT: Hiltz, William D.

APPLICANT: Kinney, Anthony J.

APPLICANT: Rafaleki, Antoni

APPLICANT: McGonigle, Brian

APPLICANT: Lohman, Karin

TITLE OF INVENTION: Enzymes Involved In Squalene Metabolism

FILE REFERENCE: B1113 US NA

CURRENT APPLICATION NUMBER: US/09/419,679

EARLIER FILING DATE: 1999-10-15

EARLIER APPLICATION NUMBER: 60/105,405

EARLIER FILING DATE: 1998-10-23

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Microsoft Office 97

SEQ ID NO 1

LENGTH: 2558

TYPE: DNA

ORGANISM: Zee maye

US-09-419-679-1

Query Match 46.2%; Score 1183.6; DB 3; Length 2558;

Best Local Similarity 72.2%; Pred. No. 0;

Matches 1540; Conservative 0; Mismatches 594; Indels 0; Gaps 0;

Qy 184 ACCCAACAAACAGCCGCTGATCTATTATCCGATGAGTGGCGAAGAGAAACCAACA 243
Db 3 ACCAGCAAGCAGCCGCCGACCTCTCATGCGCATCGATCCCAAGAAACCTGATT 62
Qy 244 CGTGAAGTCTTGGCCAAAGCGGAGTTAAGATATTGAGATGAGACCCCAAGATTGTG 303
Db 63 GAGCTTCACTTCCAGGCATCAAGCTCGGTGAGCATGAAATGTGACCGAGAACTGTG 122
Qy 304 ACAAACAATTAAAGAGGCGCTAAGTTTCATTCACTCTCCAGTGCATGACGAGAC 363
Db 123 TTGACATCACTTAAAGAGGCAATCAAGCCGTTTCTTCACTCTCCAGGCAATGATGAGAC 182
Qy 364 TGGCCCGGAGATTATGAGAGTCCCATGTTTCTGATGCTGGCTTGGTAATTAATCTGTCT 423
Db 183 TGGCTCGGGATTAATGAGTGTGCTTATGTTCTTAATGCAAGCTTGATCATTAATGATTGTAT 242
Qy 424 ATACACTGGGGCGTTGAATACAGTCTTAATGAAAGACATGAAGAAAGAAATATGCCGTAC 483
Db 243 GTACACTGAGCACTAAACACTGTCTTGTCAATGGAAACCAAGAAAGAAATCCCGGTAT 302
Qy 484 CTCTAATATCATCAAAACAAGATGAGTGGGTGGGTGGATATTGAAGGTCCAGACAC 543
Db 303 CTTTATATATACACAGATGAAGATGGCGGTGGGGCTTGCACATGAGGGTCCAGACAC 362
Qy 544 ATGTTTGGCTCTGTCTTGAATTATTAATCTGAGATTGCTAGTGAAGGGGCTTAATGAT 603
Db 363 ATGTTTGGCTCTGAGCACTGACCTATGTTATTTGAGATTGCTTGAAGGAGCAAGATGAT 422
Qy 604 GGAACAAGGGAAATGAGAAAGGACGTGATGATTTCTAAGGCACTGGTGGTCTACTTAT 663
Db 423 GGAATATGAGCCATGGAGAAAGTTCGAACCTGATATTAGACCATGGTGAAGACATAT 482

Qy 664 ATAACTGATAGGAGAGATGAGCTTCAAGTACTTGAGATGATGAATGCTGTGAAAT 723
Db 483 ATAACTGATAGGAGAGATGAGCTTCAAGTACTTGAGATGATGAATGCTGTGAAAT 723
Qy 724 AATCCCTGCCCCCTGAGATATAGCTCTTCCATACATGCTTCCATTCATTCAGAGAG 783
Db 543 AACCCGGGCGACAGAAAGTATGCTACTGCAATCTCTCCATTCATTCAGAGAGAG 602
Qy 784 ATGAGTGTCACTGCCCGAGTGTCTATTGCGGATGCTCTACTTATATGAGAGAGTTT 843
Db 603 ATGAGTGTCAATGTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 662
Qy 844 GTTGGTCAATCTCCAAACAGATATATCTTGAAGAAAGAGCTTATACATACATAC 903
Db 663 GTTGGTCAATCTCCAAACAGATATATCTTGAAGAAAGAGCTTATACATACATAC 722
Qy 904 CATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 963
Db 723 AGCAAGATTTGATTTGAGCAAGGCGCGCAACCTATGTCAGAGAGATCTGATACCA 782
Qy 964 CACCACTTGTACAGAGATATCTTGGGATCTTACACAGTCTTGAAGCTTATCTG 1023
Db 783 CACCACTTGTACAGAGATATCTTGGGATCTTACACAGTCTTGAAGCTTATCTG 842
Qy 1024 ATGCAATGGCCCGAAGAAAGATTTGAGGAAAGAGCTATATTTCTGATTTGAGCATATA 1083
Db 843 ATGCAATGGCCCGAAGAAAGATTTGAGGAAAGAGCTTGAAGAGCTATGCAATGAT 902
Qy 1084 CATTACGAGATGAGATATCTGATATATTTGATCATGATCTGATATATTAAGGTATTAAT 1143
Db 903 CATTACGAGATGAGATATCTGATATATTTGATCATGATCTGATATATTAAGGTATTAAT 962
Qy 1144 ATGCTTGTCTGTGGTGGAGATATCCAAATTTGAGGCTTCAAGTTCATCTTCCAG 1203
Db 963 ATGCTTGTCTGTGGTGGAGATATCCAAATTTGAGGCTTCAAGTTCATCTTCCAG 1022
Qy 1204 ATTTATGATATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1263
Db 1023 GTCTATGATATCTTGTGGTGGAGATGATGATGATGATGATGATGATGATGATGATGAT 1082
Qy 1264 CAACATGAGGACACTGCTTGTGCTGCAAGCAATTTGATGATCTTAACCTCATTAAGAA 1323
Db 1083 CAACATGAGGACACTGCTTGTGCTGCAAGCAATTTGATGATCTTAACCTCATTAAGAA 1142
Qy 1324 TTTGATCAACTATTAAGAAAGCTCATATATTAAGATTTCAAGGTTTGAAGAT 1383
Db 1143 TTTGATCAACTATTAAGAAAGCTCATATATTAAGATTTCAAGGTTTGAAGAT 1202
Qy 1384 TGTCCAGTGTATCTTAATTAAGATGATGATGATGATGATGATGATGATGATGATGAT 1443
Db 1203 TGTCCAGTGTATCTTAATTAAGATGATGATGATGATGATGATGATGATGATGATGAT 1262
Qy 1444 ACTGAGATCATGATGAGGCAATTTCTGACTGCAAGCTGGAAGGATGGAAGCTGTTCTTA 1503
Db 1263 ACTGAGATCATGATGAGGCAATTTCTGACTGCAAGCTGGAAGGATGGAAGCTGTTCTTA 1322
Qy 1504 TTAATATCAAAATTTCAACAGAAATAGTTGTGAGCAATAGACGTGAAGCGATTATAT 1563
Db 1323 TTAATATCAAAATTTCAACAGAAATAGTTGTGAGCAATAGACGTGAAGCGATTATAT 1382
Qy 1564 GATTCGTGAATGTCAATCTCTCACTACAGAAAGATGATGATGATGATGATGATGATGAT 1623
Db 1383 GATTCGTGAATGTCAATCTCTCACTACAGAAAGATGATGATGATGATGATGATGATGAT 1442
Qy 1624 CTTAAAGATCTTATATATGTTTGAAGATATCAATCTGCTGAACCTTTTGTGATCATC 1683
Db 1443 CTTAAAGATCTTATATATGTTTGAAGATATCAATCTGCTGAACCTTTTGTGATCATC 1502
Qy 1684 GTTATGATATATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1743
Db 1503 GTTATGATATATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1562
Qy 1744 AGGAATATATCTTGTGGGATGCGCCAGAAAGAAATCAACATTTGTATGATTAAGCACT 1803

Db 1563 AAAAATCATATACCTGGGACCGGACGAAAGGGTGATTAATCTGATATACGAAAGCTTCC 1622
Qy 1804 ACCTTCATTAAGAAAATACAAAGCTTCAATGATCATGTATGTCTTCTGGGAGATTGC 1863
Db 1623 AATTTCATCGAGATTCAGAAAAGCGATGTTATGTATGTCTTCTGGGAGCTTCTGT 1682
Qy 1864 TTCACTTACGGTGTGGTGGGTAAAGGTCGATTTGCTGCTGGAAGAGTTTCAGT 1923
Db 1683 TTTCATATACGACATCTGTTGTGTGTGTGAAGGACTTAATGCTGCTGTGTGAACAATTGAG 1742
Qy 1924 AATTGCTCAAGCATCCGTAAGCTTGTGAATTTCTGCTGTCCAGACGCTTCTTCTGT 1983
Db 1743 AACAGTCTGCATATAGAAAAGCATGCGACTTCTGTGTCAAAAAGACTTCTTCCGCT 1802
Qy 1984 GCGTGGGAGAGAGTATCTGTCTGTCAAAAAGGTTATTCAAATCTGGAAGGCAAC 2043
Db 1803 GGTGGGAGAAAGCTAATTTGTCTCATCTCAAGACAGTTTATCACTCAATCAATCAGAG 1862
Qy 2044 AGGTCTCATGTGTCAACACTGGGTGGGCTATGTTGGCTCTCATTTGATGTGSAAGGCT 2103
Db 1863 CCGCTCATGTGGGTAAACATGTTGGGCTGCTGCTGCTGATTTGATGCGGCGCAAGCC 1922
Qy 2104 AAGAGATTCGCAACCACTGCAAGGCGGCACTGTCATTTGATTAATTTCCCAATTGGAG 2163
Db 1923 GAGAGATTCCAAGGCTCTACACGAGCAGCAAGTTTGTATCACTTCAATCAATCAGAG 1982
Qy 2164 GACGCTGATTTCCGACAGAAATTAATGGAGTCTTCAACAAATTTGATGATCA 2223
Db 1983 GACGAGATTTCTTCAGCAAGAGATCATAGAGTGTTCACMAAATCTGATGATTAAGC 2042
Qy 2224 TACGCGCATACAGAAATATTTCCCATTTGGGCGTTGGGAGAAATACCAATCCCAATGA 2283
Db 2043 TACTCCAGTACAGAAATCTTCCCATTTGGGCTCTGGGAGTACCGGTGTGAGTC 2102
Qy 2284 TTGCAATCTCGTTAATGAGCCTTAAGTAAAGGCTG 2317
Db 2103 TTGGGGGCTGGCAAGCTTTGGCGGTGAACGGGAG 2136

RESULT 3
US-09-419-679-3
; Sequence 3, Application US/09419679
; Patent No. 6630617
; GENERAL INFORMATION:
; APPLICANT: Falcoy, S. Carl
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Rafalski, Antoni
; APPLICANT: McGonigle, Brian
; APPLICANT: Lohman, Karin
; TITLE OF INVENTION: Enzymes Involved In Squalene Metabolism
; FILE REFERENCE: B0113 US NA
; CURRENT APPLICATION NUMBER: US/09/419,679
; EARLIER FILING DATE: 1999-10-15
; EARLIER APPLICATION NUMBER: 60/105,405
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-419-679-3

Query Match 36.9%; Score 944; DB 3; Length 1882;
Best Local Similarity 74.4%; Pred. No. 1,56-277;
Matches 1190; Conservative 0; Mismatches 410; Indels 0; Gaps 0;

Qy 687 GCTTCACTACTGAGTGTATGAATGTCTGGAATATATCCCTGCGCCCTGAGATATG 746
Db 14 GCTTCCGTCGCTGGTGTATTTGACTGGCTGGCAACCAACGATGCGACCAAGAAATATG 73

Qy 747 GCTCTTCATATACGCTTCCATTTCAATCCGAAAGATGTGTCACTCCGGATGCT 806
Db 74 GTTGTGCAATATTTCTGCGGATTTCAATCCAGGCGAATGTGTCTATTTCCCGATGCT 133
Qy 807 CTATTTGCCGATGTCTCATTTATATGCGAAGAGTTTGTGTCTCAATCTCAGCAACGT 866
Db 134 TTAATTCCTATGTGTATACATTTATGAAAGAGTTGTGGGCCCAAGTTATACCAATAT 193
Qy 867 ATATATCTTGAAGAAAGCTTTTATACATACATACATACATACATACATACATACAT 926
Db 194 ATTGAAATTAAGAAAGAACTTACGAAGTACCTTACAAAGTGAATGATTTGACCAAGC 253
Qy 927 TCGCAATTTGTGTCAAGAAAGATTTGTACTATCTCAATCCACTGTGACAGATATCT 986
Db 254 TCGCAATCTATGTCTTAAAGAAAGTCTGTACTATCCATCTCATTTGCTGAGATAT 313
Qy 987 TTGGGCACTCTTACCAAGATTTCTTGAAGCTTATCTGATGATTTGGCTGGAAAAAGTT 1046
Db 314 ATGGGCACTCTCACAATAATTTGTTGAACGATATGTGGCTGGCTGGGAAACAATTT 373
Qy 1047 GAGGAAAAAGCTATTTATTTGTGATGTGACATATACATTAAGAAATGAAATATCTG 1106
Db 374 GAGGAGAAAGCTTTGACATCTGATGACAGCATATTCATTAAGATGAGAACACCG 433
Qy 1107 ATATATTTGCACTAGCTCTGTAAATTAAGTGTAAATATGCTTGTGTGGTGAAGA 1166
Db 434 ATATATTTGCACTGTGTCAATGAAAGATTTAAATATGCTTGTGTGTGATTAAGA 493
Qy 1167 TCCAATTTGAGGCTTCAAGTTGATCTTCCAGAGATTTATATTAATTAATGATG 1226
Db 494 TCCAAATCTCAGAGCATTTCAAACTCCACATTTCAAGATCCACATTTACTATGATG 553
Qy 1227 AGAAGATGCAATGAAATTAAGGCTCAATGAAAGTCAATAGGACATGCTTTTGC 1286
Db 554 AGAAGATGCAATGAAATTAAGGCTCAATGAAAGTCAATAGGACATGCTTTTAC 613
Qy 1287 TGTCCAAGCAATTTATGATCTAATCTCAATGAAATTTGCTCAATATAGAAAGC 1346
Db 614 AGTTCAAGCTATATGTGCTATGCTGCTCATTTGAAAGATTTGTCTACTTTAAACTAGC 673
Qy 1347 TCATACCTAATTAAGAAATTCACAGGTTTGAAGATTTGTCAGGTGATCTTAATTAATG 1406
Db 674 ACATGGCTACATTAAGAAAGCAGGTTATGATGATGCTGCTGAGATCTTATGATG 733
Qy 1407 GTACCTGCAATTTCAAAAGGTGCTTTTCACTGAGAAATCATGATGATGAGCCAAAT 1466
Db 734 GTACCGCACTATCTAAAGGTGATGCTCTTTTCACTGATCATGATGATGATGATG 793
Qy 1467 TTGCACTGCACTGAGAGAGTGAAGCTGTTCTATTAATCTCAAAATTTGACACAGA 1526
Db 794 ATCAGATTTGCACTGCAAGAGAGCTTAAGCGGCAATTTGCTATCGAAGATTTCTCCAGA 853
Qy 1527 AATAGTTGTGAGCAATTAAGCGTGAAGCATTAATTAATTTCTGTAATGTCTCTG 1586
Db 854 TATTTGGCGAAGCAGAGGAAATTAAGCTGATGATTTCTGCAATTTGATGATGTC 913
Qy 1587 ACTACAGAAATGAAGATGTGTGTTTGAACATTAAGCTTAAAGATCTTAATTTGTT 1646
Db 914 ATACATGAATGATATGTGTGATTTGCAACATTAAGCTTAAAGCTTAAAGCTTAAAG 973
Qy 1647 GGAGATTAATCAATCTGCTGAAACTTTTGGGACATGCTTATGATTAATCTTATGTTGA 1706
Db 974 GAGCTTATCAATCTGCTGAGACCTTTGGGACATGCTTATGATTAATCTTATGTTGA 1033
Qy 1707 ATGTACATACAGCAAGATTCAGCTTTGGCATCTTAAGAAATTAATCTCTGGCAATG 1766
Db 1034 ATGCACTTACAGCAATTTACGCTTGAAGCATTTTAAAGCTTAACTCTGAGACCG 1093
Qy 1767 CCGAAGAAATTAACATTTGATGATTAAGCACTTACCTTCAATGAAATTAACAGC 1826
Db 1094 CAAGATGAATTAACATCTGATTAAGCAAGCTTATGAGGCTTATTAAGGCTTATTAAG 1153

Qy	1827	TTGAGATGATCATGATATGTTCTTGGGGAGTTTGCTTCACTTAACGGTCTTGATTTGG	1886
Db	1154	AAGCGATGTTCAAGTATGGTCTTGGGCGTTTGTTTTACCTATGGCACAATGGTTGG	1213
Qy	1887	GGTAAAGGTCGATTGCTGCTGGAGAGGATTCAGTAAATGCTCAAGCATCCGTAAGC	1946
Db	1214	TGTAAGGGATTAGTGTGCTGCTGGAGACATTCAAAGACAGTCCGCAATCAAGAAAGGC	1273
Qy	1947	TTTGGAATTTCTGCTGTCAGACAGCTTCCTTGCGGGCGAGGAGAGATTTATCTGTC	2006
Db	1274	ATGAGACTTTTGTGTCAAAAGACTTCTTCTGGAGGCTGGGGAGAAACCTATTTGTCTC	1333
Qy	2007	CTGTCAAAACAAGGTAATTCMAATCTGGAAGCAACAGTCTCATGTGTCAACACTGG	2066
Db	1334	ATCCCAAGATCAGGTTTATTAACAATCTCGAAGGAAAGCACTCATGCGGTAAACACTGG	1393
Qy	2067	GTGGGCTATTTTGGGCTCTCATTTGATGCTGGACAGGCTAAAGAGATTTGGCAACAACCTGCA	2126
Db	1394	TTGGGCACTGCTAGGCCCTPATTCGATGACAGGGCGAGGCTAAGAGATTCMAATTCCTTGCA	1453
Qy	2127	CGGGGACGCTGCATCTGATTAAATTTCCCAATTGGAGAGCGGTGACTTTCCGACAGAGA	2186
Db	1454	TCGAGCAGCGAAGGTTTGTATCACTTACATTCGGAATATGTGAATTTTCCGACAGAGA	1513
Qy	2187	AATAATGGGAGTCTTCAACAAGATTGCATGATCATACGCCGCAATCAAGAAATATTT	2246
Db	1514	GATCATTTGAGACTTCAACAAGAAATCGCATGATCTCCGATATAGAAACATCTT	1573
Qy	2247	CCCACTTTGGGCGTTGGGAGAATACCAATCCCAAGTATTTG	2286
Db	1574	CCCTATTTGGGCGCTTTGGGAGATCCGTCGCGGCTTTG	1613

RESULT 4
US-09-419-679-7
; Sequence 7, Application US/09419679

```

/ GENERAL INFORMATION:
/ APPLICANT: Falco, S. Carl
/ APPLICANT: Farnodu, Omolayo O.
/ APPLICANT: Hitz, William D.
/ APPLICANT: Kinney, Anthony J.
/ APPLICANT: Rafalski, Antoni
/ APPLICANT: McGonigle, Brian
/ APPLICANT: Lohman, Karin
/ TITLE OF INVENTION: Enzymes Involved In Squalene Metabolism
/ FILE REFERENCE: B8113 US NA
/ CURRENT APPLICATION NUMBER: US/09/419,679
/ CURRENT FILING DATE: 1999-10-15
/ EARLIER APPLICATION NUMBER: 60/105,405
/ EARLIER FILING DATE: 1998-10-23
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: Microsoft Office 97
/ SEQ ID NO: 7
/ LENGTH: 1300
/ TYPE: DNA
/ ORGANISM: Triticum aestivum
/ US-09-419-679-7

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Query Match	22.0%;	Score 563.8;	DB 3;	Length 1300;
Best Local Similarity	72.2%;	Pred. No. 2.2e-161;		
Matches 733, Conservative	0;	Mismatches 282;	Indels 0;	Gaps 0;

QY 1272 GGAACACTGGTTTTGCGTCGCAAGCAATTATTCGATCTAAACCTCATTTGAGAATTTGGTCC 1331

Db 7 GGAACAGAGTTTTTGACGTTCAAGACTCTTTGCGGCACATGACCTCATTTGAGAAGTTTGGTCCC 66

QY 1332 AACTATPAGAAAAGCTCATACCTATATTAAGAAATTCACAGTTTTAGAAGATTGTCCAGG 1391

Db 67 CACTCTTAAGCTGGGACATGATTTTATTAAGAACTCTCAGGTGTGTGATGACGTCCCTGG 126

QY 1392 TGAATCTTAATAATGATACCGTCACATTTCAAAAGTGCTGGCCTTTTCAACCTGGAGA 1451

Db	127	AGATCTGATTACTGTAACGGTCAATATCTAAAGGTCATGGCCCTTTCTACAGCTGA	186
Qy	1452	TCATGATGCGCAATTTCTGACTGCACTGCAAGCTGAAGACCTGAAGCTGTCTATTAATC	1511
Db	187	TCATGTTGGCTTATATACGATTTGCACCTGCAAGAAGACTAAAGCCCTCATTAATGCTATC	246
Qy	1512	CAAAATTGCACACAGAATATGTTGGTGCCATAGACGTGAACGATTAATATGATCTGT	1571
Db	247	AAAGATTTCTTCAGAAATTTGTGGCCGAATGGGTGGAAGTTAACAGACTAATATATGTCT	306
Qy	1572	AAATGTCATCTCTCACTACAGAAATGAAGATGCTGTTTTCACATATGAGCTTAAACG	1631
Db	307	CAATTGTTGATGCTTGGATGATGAAATATGGTGGCTTGGCAACATATACCTCCAAAG	366
Qy	1632	ATCTTAATATGTTGATGAATATCAATCCGTGCGAAACCTTTGATGACATCGTATTTGA	1691
Db	367	GTTTATGCTGGGCTTAGCTTATCAACCTGCCAGACATTTGGAGATATTTGTGATTTGA	426
Qy	1692	TTATCTTATGTGATATGATACATCAGACGAGATTCAGACTTTGGCATTTTAAAGAAAT	1751
Db	427	TTACCCGTAATGTAATGTACCTCAGCGCAATTCAGGCCCTGACATCATTTAAAGAACT	486
Qy	1752	ATATCTGGGATGCGCGAGAAATATCAACATTTGATGATTAAGCCACTACCTCAT	1811
Db	487	CTATCTGGGACCGCAGAAAGATGATATCACTGATCAACAAACCTGCTAGTTACAT	546
Qy	1812	TGAAAAAATACAGACTTCAGATGATCATGATATGTTCTTGGGGAATTTGCTTCACTTA	1871
Db	547	TGAGAGATCCAAAGAAAGATGTTATGTATATGCTCTTTGGGCTGTGTCTTCACTGA	606
Qy	1872	CGGTGCTTGGTTTGGGTTAAAGGTCTGATTTGCTGCTGGAAGAGTTTCAGTATTTGCTC	1931
Db	607	TGGCACATGTTCCGAAGTGAAGGGGCTTACTAGCTGCAAGATGAACCTTCAAGACACTCC	666
Qy	1932	AAGCATCGTAAAGCTGTGAAATTTTGTGCTGTCCAAAGAGTTCTCTTGTGGGCTGGG	1991
Db	667	TGCATTCAGAAAGGATGTGACTTTCTGATGTCAAAGAGCTTCTTTGGTGGCTGGG	726
Qy	1992	AGAGAGTATCTGTCTCTCTCAAAAACAAGTATTTCAAATCTGGAAGGCAACAGTCTCA	2051
Db	727	AGAAAGCATCTGTCTCATCTCAAGATCAGGTTTACACCAATCTTGAAGGAAAGCATCTCA	786
Qy	2052	TGTGTCAACACTGGGTGGGCTATTTGGTCTCAATGATGCTGGAAGAGGTTAAGAGA	2111
Db	787	TGCTGTCAACTGTGCTGGGCAATGTGACTCTTAATTTGACGACAGACAGGCTGAGAGGA	846
Qy	2112	TTTCGCAACACTGCACCGGGAGCTGCATACTTATTAATTTCCCAATTTGAGAGACGATGA	2171
Db	847	CCCGACGCTCTGCATTCAGACAGGAGAGGTTTGATTAACCTTACATCAGAGATGGGGA	906
Qy	2172	CTTTCGAGACAGAAATATAGGAGTCTTCAACAAGATTCATGATCACTACGCGC	2231
Db	907	ATTTCTCAGCAAGATCATGGGAGTCTTCAACAAGAACATGCATGATCACTACTCCA	966
Qy	2232	ATACAGAAACATTTCCCATTTGGGGCTTGGGGAATACCAATCCCAAGATTTG	2286
Db	967	GTATCGAAACATCTTCTTATCTGGGCGCTTTGGCGAGTACCGCTCCGGGTGCTG	1021

RESULT 5
US-09-919-039-112

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? Sequence 112; Application US/00222.113
? Patent No. 6727066
? GENERAL INFORMATION:
? APPLICANT: Kaser, Matthew R.
? TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
? FILE REFERENCE: PA-0035 US
? CURRENT APPLICATION NUMBER: US/09/919,039
? PRIOR FILING DATE: 2002-09-09
? PRIOR APPLICATION NUMBER: 60/222,113
? PRIOR FILING DATE: 2000-07-28
? NUMBER OF SEQ. ID NOS: 401
? SOFTWARE: PERL Program

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SEQ ID NO 112
LENGTH: 4346
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Inbyte ID No. 6727066 225080.16
US-09-919-039-112

Query Match 11.9%; Score 304.8; DB 3; Length 4346;
Blast Local Similarity 51.4%; Pred. No. 7.2e-82;
Matches 997; Conservative 0; Mismatches 877; Indels 66; Gaps 10;

Qy 343 CTCGATCCATGACGACATGCGCGGAGATTATGAGGCCATGTTCTGATGCT 402
Db 417 CTGACGCGTGAGATGAGCATGAGCGGATATATGATGCGCCACTTTCTCTGCA 476
Qy 403 GGCCTTGTAATTAATCTGCTATCACTGCGGCGTTGAATACAGTCTTAAGAAACAT 462
Db 477 GGCCTCTGATCACTTGCCAGTGCAAGC-----ATCCCTCTGCGAGCGGATAC 527
Qy 463 AGAAGAAATATGCGCTTACTCTATATATATCAAAACAGATGCGGCTGGGTTG 522
Db 528 AGAAGAGATTTGCGGATCTGCGATGAGTGCCTGACGCGTGGGCTG 587
Qy 523 CATATGAGGTCCAGACCATGTTTGGCTCTGCTTGAATTATTAATCTGAGATG 582
Db 588 CACATTGAGATTAATGTCACCGCTGTTGGACTGCGCTCACTATGCTCTCTAGATT 647
Qy 583 CTAGGTGAGGGGCTTAATGATGACAGAGGAAATGAGAAAGCACTGACTGATCTA 642
Db 648 CTGGGTGTTGGGCTGACGAT-----CTGACCTGTACGAGCCCGGAACATTCTTAC 701
Qy 643 GGGCATGTGTGCTACTATATATACCTCATGGGGAAAGATGCGCTTCAGTATGGA 702
Db 702 AAGAAAGGTGTGTGCGCCATCCCTCTGCGGAAAGTTCTGCGCTGCTGAAAT 761
Qy 703 GTGTATGATGCTGGAATATATCCCTGCCCCGATGATGAGCTCTTCCATACATG 762
Db 762 GTTTACAGCTGGAAAGGCTCAATACCTGTTCCAGAGATGAGCTGTTCTTGACG 821
Qy 763 CTTCATTTTCATCCAGAGAGATGTGTGTCATGCGCGATGATCTATTTGCGCATG 822
Db 822 GCACCGGACACCCCTCACACTCTGTGTGACATGCGCGAGGTGATCTCCCATGAGC 881
Qy 823 TACTTATATGCGAAGAGTTTGTGTGCAATTCACCAAGATATATCTTTGAGAAA 882
Db 882 TACTGCTAACCGCTTGGCTGAGTGCAGGAGAACCGCTGTGTCAGAGCTCCGCG 941
Qy 883 GAGCTTATACAGTACCATCATGATATAGATTGGATCAGGCTCGCAATTTGTGCA 942
Db 942 GAGCTTATGAGAGACTTGGCCAGCATTTGATGCTGCGCGAGAGAACAGTGGCC 1001
Qy 943 AAGAGAGATTGTAATCTCTCACCCACTTGTACAGATATCTTTGGGCACTCTAC 1002
Db 1002 CCCGACGAGCTGACAGCGCCCAAGCTGCTGCTCGCGGTGATATGCGCTCTCAC 1061
Qy 1003 AAGTTCCTGAGCTATTTCTGATGCTTGGCTGAGAAAGATGAGGAAAGGCTATT 1062
Db 1062 CTGTA-----TGACACCAACACAGTGCACCTGCGCAGCGGCGCTG 1106
Qy 1063 ATTTCGATTTGAGCATATATCATTTAGAGATGAGATCTGATATTTTGGATGGT 1122
Db 1107 CAGAGAGCTATGAAACATTTGTGGCCGACGACGATTCACCAAGAGATCAGATGGC 1166
Qy 1123 CCGTAAATAGAGTGAATATGCTT---TGCTTTGGGTGAGAAATCCAAATTTGAG 1179
Db 1167 CCGATTCGAAAAACATCAACATGCTGTGTGCGTGTATGTGAGCGGCGCGCTCACT 1226
Qy 1180 GCTTTCAAGTTGATCTTCCAGATTTATGATATCTATGATGCGAAGATGCGATG 1239
Db 1227 GCTTTCAAGGAGCATGTCTCCAGAAATCCCGGATATCTCTGATGCGGCTTGAAGGATG 1286

Qy 1240 AAAATGACGGGCTACAAATGAGTCAACTATGAGCACTGCTTTTGTGTCAGCAATT 1239
Db 1287 AAAATGACGGGCAACCAACGGGTACAGATCTGGGACACCGGATTCGCAATGAGCTCTG 1346
Qy 1300 ATTGCATC-----TAACCTCATTTGAAAGATTGCTCAACTATAGAAAAGCTCATCC 1353
Db 1347 CTGAGCGCGGCGGCGACCAAGCGCCGAGTTTCTGCTGCGCTGCAAGAAAGGCTCATGAG 1406
Qy 1354 TATATTAAGAAATTCACAGGTTTTAGAGATTTGTCAGGTATCTTAATATGATACCGT 1413
Db 1407 TTCTGAGGCTTTCACAGGTTCCAGATTAACCTCCGACTAC--AGAACTACTGCGC 1463
Qy 1414 CACATTTCAAAAGGTGCTGGCCCTTTTCACTGAGATATGATGAGGCCAATTTCTGAC 1473
Db 1464 CAGATGGCAAGGTGGCTTCTCTTCAAGTACGTGACCTGCGGTGATGCTTTCTGAC 1523
Qy 1474 TGACAGCTGAAAGACTGAAAGCTGTTCTATTAATATCAAAATTTGACCGAATAAGTT 1533
Db 1524 TGACGCGCTGAGGCTTGAAGGCTGTGCTCTCTGCGAGAGAGTGTCCCAT---GTC 1580
Qy 1534 GGTGAGCCATTAAGACGTGAAGCATTAATGATTTGTAATGTCATTTCTCTCATAG 1593
Db 1581 ACCGAGCATCCCGACAGAACGCTCTGCAATGCTGTGCTGTGACATGAGA 1640
Qy 1594 AATGAAGATGATGATTTTGGACATATGAGCTTAAACGATCTTAATATGTTGAGATA 1653
Db 1641 AATTCAGATGAGAGTTTGGCACTATAGAACCAAGGTGGGGGCACTTGTGACTG 1700
Qy 1654 ATCAATCTGCTGAAACTTTTGTGATGATGTTATGATTAATCTTAATGTGAAATGTA 1713
Db 1701 CTGAACCCCTCGAGAGGCTTTCGAGGACATCATATGACTATACACTATGTGAGTGCAC 1760
Qy 1714 TCAGAGCGATTCAGAGCTTTGGCATATTAGAAATTAATCTCGGCAATCGCGGAA 1773
Db 1761 TCAGCGGATGACAGGCGCTTAAGTATTTCAACAAGCTTTCCCGAGCAAGGCGCG 1820
Qy 1774 GAAATACAACTTATATGATATGATTAAGCACTACCTTCAATGAAAAATACAACTTCAGAT 1833
Db 1821 GAGATCCGGAGAACCTCAGCGAGGCTTAGAGTTCTGTGGCGGACAGAGGCGGAT 1880
Qy 1834 GATCATGTATGATTTCTTGGGAGATTTGCTTCACTTACGCTGTGTTTGGGATAA 1893
Db 1881 GGCCTCGGAGAAAGCTCTCGGAGATTTGCTTCACTTACGCGCACTGTGTTGGCTGAG 1940
Qy 1894 GGTCTGATCTCTGGAAGAGTTTCAGTAAT-----TGCTCAACATCCGTA 1944
Db 1941 GCTTGGCTGTATGAGGACACTTACCGAGATGGAATGCTGTGTGAGAGTCTCCCG 2000
Qy 1945 GCTTGTGAATTTTCTGCTGTCCAAGCACTTCTTGTGGCTGGGAGAGATTAATCTG 2004
Db 2001 GCTGTGATCTTCTGCTGTCCCGCAGATGAGCAGACGAGGCTGTGGGAGAGACTTTGAG 2060
Qy 2005 TCTGTCAAAAACAAGGTATTTCAAACTTGAAGGCAACAGTCTCATGTGTCAACACT 2064
Db 2061 TCTGCGAGAGAGGCGGTATT-----TGCAAGATGCCAGTCCGATTCATTAACA 2114
Qy 2065 GGGTGGCTATGTTGGCTCTCATTTGATGCTGACAGGCTTAAGAGATTTGCAACACTG 2124
Db 2115 TGCTGGGCAATGATGAGGCTGATGCGCTTGGCATCTTCAATCGAGGCCA-----G 2168
Qy 2125 CACCGGACAGCTCATCTTGAATTAATTTCCCAATTTGAGAGCGGTGACTTTCCGACAG 2184
Db 2169 GAGAGAGAGTCCGGTGTCTATTTGAGAAACAGCTCCCAATGCGACTGCGCGAGAA 2228
Qy 2185 GAAATATAGGAGTCTTCAACAGAAATTTGATGATCAATACGCGCATACAGAAATTA 2244
Db 2229 AACTATGCTGGGCTTTCAACAGATCTGTGCTGATCTCTTACACAGACTACAGAAATC 2288
Qy 2245 TTCCCATTTGGCGGTTGGG 2264
Db 2289 TTCCCATTTGGCGGCTCGG 2308

```
RESULT 6
US-09-815-048-1
/ Sequence 1, Application US/09815048
/ Patent No. 6737261
/ GENERAL INFORMATION:
/ APPLICANT: WEI, Ming-Hui et al.
/ TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
/ TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
/ TITLE OF INVENTION: THERBOF
/ FILE REFERENCE: CL001180
/ CURRENT APPLICATION NUMBER: US/09/815,048
/ CURRENT FILING DATE: 2001-03-23
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 4239
/ TYPE: DNA
/ ORGANISM: Human
US-09-815-048-1

Query Match      10.9%; Score 280.2; DB 3; Length 4239;
Best Local Similarity 51.4%; Pred. No. 2,4e-74;
Matches 906; Conservative 0; Mismatches 798; Indels 57; Gaps 9;

Qy      522 GCATATGGAAGTCCAGACACATGTTGGCTCTGCTTGAATTATTAATCTGAGATT 581
Db      429 GCATATGGAAGTCCAGACACATGTTGGCTCTGCTTGAATTATTAATCTGAGATT 488
Qy      582 GCTAGTGAAGGAGGCTTAATGATGAGACAGAGGAAATGAGAAAGGACGTGACGATTCT 641
Db      489 TCTGGGTGTTGGGCTGACGATCTCT-----GACCTGTGACGAGCCCGGAACATCTTCA 542
Qy      642 AGGGACATGAGTGTGCTACTATATTAAGTCAATGAGGAGAGATGAGCTTTCAGTACTG 701
Db      543 CAAGAAAGGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 602
Qy      702 AGTGTATGATGTGCTGGAATATATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 761
Db      603 TGTTTACAGCTGGAGAGGCTCAATACCTGTTCCGAGATGTGCTGTTCTGACATG 662
Qy      762 GCTTCATTTTCAATGAGAAAGATGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 821
Db      663 GGCACCGGACACCCCTCCACACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 722
Qy      822 CTACTATATGGAAGAGTGTGTGTGCTGCAATCTCAACAGATATATCTTTGAGAAA 881
Db      723 CTACTGTACGCGCTTGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 782
Qy      882 AGAGCTTTATACATGACATACATGATATGATGATGATGATGATGATGATGATGATG 941
Db      783 GAGCTTATGTGAGAGACTTCCGACATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 842
Qy      942 AAGAGAGATTTTACTATCTCTCACTGCACTTGTACAGAGATTTCTTTGGCAGTCTCA 1001
Db      843 CCCCGAGAGCTGTACAGCGCGCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 902
Qy      1002 CAAGTTCCTTGAAGCTATTTCTGATGATGATGATGATGATGATGATGATGATGAT 1061
Db      903 CTGTGTA-----TGAGCACACACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 947
Qy      1062 TATTTGATGATGAGCATATATCATTTAGAGATGAGAAATCTGATATATTTGCAATG 1121
Db      948 GAGAGAGCTGTATGACATATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1007
Qy      1122 TCTGTAAATTAAGGTGTTAAATATGCTT---TGTGTGTGTGTGAGAAATCTCAATTT 1178
Db      1008 CCCGATCTGAAAACCAATCAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1067
Qy      1179 GGCCTTCAAGTTGATCTTCCAGAGATTTATGATTTATGATTTATGATTTGAGAAATG 1238
Db      1068 TGCCTTCCAGAGAGATGTCTCCAGAAATCCGGAATATCTTGTGATGAGCTTGAAG 1127
Qy      1239 GAAATGACAGGCTTACATGAGATCAATATGGAACATGCTTTTGTGTGCAAGCAAT 1298
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Db      1128 GAAATGACAGGCTTACATGAGATCAATATGGAACATGCTTTTGTGTGCAAGCAAT 1187
Qy      1299 TATTGATC-----TAACCTCATTTGAAGATTTGTGTGCAATTTAAGAAAGCTCATAC 1352
Db      1188 GCTTGAAGCGGCGGAGGACCAAGCGCCGAACTTTTGTGTGCTGCTGCAAGAGGCTCATG 1247
Qy      1353 CTATTTTAAGAAATTCACAGGTTTGAAGATTTGTCCAGAGTATCTTAATAATGTTACCG 1412
Db      1248 GTTCTGAGGCTCTCACAGGTTCCAGATTAACCTTCCGACATAC---AGAGATCTACCG 1304
Qy      1413 TCACATTTCAAAAGGTGCTTGGCTTTTCAACTGAGATCATGATGAGTCCCATTTCTGA 1472
Db      1305 CCAAGATGAGCAAGGTGTGCTTCTCTTCAAGACGTGAGCTGCGAGTGAATCTTCTGA 1364
Qy      1473 CTGACAGCTTGAAGAGCTGAAAGCTGTTCTATTAATCTCAAAATTTGACCAAGAAATGT 1532
Db      1365 CTGACAGGCTGAGGCTTGAAGGCTGTGCTGCTCTCTGAGAGAGATGTCTCCCA---TGT 1421
Qy      1533 TGTGATGCAATTAAGCGTGAAGCGATTTATGATTTGTAATGTCATTTCTCACTACA 1592
Db      1422 CACCGAGACATCCCGAGAGAAAGGCTCTGAGATGCTGTGCTGTGCTGCTGATGATGAG 1481
Qy      1593 GAATGAAGATGAGTGTGTTGCAACATATGAGCTTAAACGATCTTAATAATGTTGAGAT 1652
Db      1482 AATTCAGATGAGAGGTTGCTGCACTATGAGCAAGGCTGAGGAGGCTGCTGAGAGCT 1541
Qy      1653 AATCAATCTGCTGAACCTTTTGTGACATGTTATTAATATCTTATGTGAGATGAC 1712
Db      1542 GCTGAACCCCTGAGAGCTTGTGAGGACATGATGATCAACCTTATGTGAGATGAC 1601
Qy      1713 ATCAGACAGATTTCAAGCTTTGGCATCATTTAAGAAATTAATCTGAGCATCTGCGAGA 1772
Db      1602 CTACAGCGGATGACAGGCGCTTAAGATTTTCAACAGGTTTCCGAGACACAGGCGAC 1661
Qy      1773 AGAAATPACAACTTGATGATTAAGCACTACTTTGAAAAATPACAGCTTCAGA 1832
Db      1662 GAGAGATCCGAGAGACCTTACAGCAGAGGCTTAAGATTTGTGTGAGGAGAGGCGCA 1721
Qy      1833 TGGATCATGATGATGATTTTGTGAGGAGTGTGCTTCACTTACGCTGCTGTTGGGTTAA 1892
Db      1722 TGGCTCTGGAAGAGGCTCTGAGGAGTTGCTTCACTACAGGACCTGCTTGTGCTGGA 1781
Qy      1893 AGGTCTGATGCTGCTGAGAGAGTTTCAATAT-----TGTCAAGCATCTGTA 1943
Db      1782 GGCCTTGTGCTGATGAGGACAGCTTACCGAATGAGACTGTGCTGACAGCTTCCG 1841
Qy      1944 AGCTTGTGAATTTTGTGCTGCTGCAAGAGCTTCTTCTGCTGCTGCTGCTGCTGCTGCT 2003
Db      1842 GGCCTGTGATCTTCTGCTGTCTCCGAGATGCAAGAGGCTGAGGAGGAGAGACTTTGA 1901
Qy      2004 GTTCTGTCAAAACAAAGTGTATTTCAATCTGAGAGGCAACAGTCTCATGTGTCAAC 2063
Db      1902 GTTCTG-----GAGAGAGGCGGTTATGTGAGAGTGTGCTGCTGCTGCTGCTGCTGCT 1955
Qy      2064 TGGGTGCTATGTTGTGCTCTCATGATGATGATGATGATGATGATGATGATGATGAT 2123
Db      1956 ATGCTGGCCATGATGAGGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2009
Qy      2124 GCACCGGAGAGCTGATATCTGATTAATTTCCAAATGAGAGGCGGATCTTTCCGACAGA 2183
Db      2010 GAGAGAGAGAGTCCGAGTGTCTACTTGAAGAAAGCTTCCCAATGAGAGTGTGCTGCTG 2069
Qy      2184 GGAATTAATGAGAGTCTTCAACAAAGATTTGATGATGATGATGATGATGATGATGATG 2243
Db      2070 AATCATTTGCTGAGGCTTTCAACAAAGTCTGTGATCTCTTACAGAGCTACAGAAAT 2129
Qy      2244 ATTCCCATTTTGGCGCTTGG 2264
Db      2130 CTTCCTCATCTGGGCGCTGCG 2150
```

RESULT 7

US-09-614-221A-308
 ; Sequence 308, Application US/09614221A
 ; Patent No. 6723837
 ; GENERAL INFORMATION:
 ; APPLICANT: Kairuanandae, Balasulojini
 ; APPLICANT: Yu, Jaehyuk
 ; APPLICANT: Kishore, Ganesh M.
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
 ; FILE REFERENCE: 16516.075
 ; CURRENT APPLICATION NUMBER: US/09/614,221A
 ; CURRENT FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/142,981
 ; NUMBER OF SEQ ID NOS: 626
 ; SEQ ID NO 308
 ; LENGTH: 2196
 ; TYPE: DNA
 ; ORGANISM: *Saccharomyces cerevisiae*
 US-09-614-221A-308

Query Match 8 2%; Score 211; DB 3; Length 2196;

Best Local Similarity 48.8%; Pred. No. 2.3e-53; Mismatches 860; Indels 54; Gaps 9;

Matches 871; Conservative 0; Mismatches 860; Indels 54; Gaps 9;

505 GATGGTGGGGGTTTGATATTTGAAGGTCAGACCATGTTGGCTGCTGTTGAGT 564
 418 GATGGTGGGGGCTGACATTCCTTGACAAATCCACCGTCTTGTCAGATATTGAC 477
 565 TATATTAATCTGAGATTGCTAGTGAAGGGGCTTAATGATGACAGAGGAAATGAGAG 624
 478 TATGTAATCTTACGTTTATTT-----GGGTACACCAAGACACCGGTTTGCCGCAAG 531
 635 GCACTGATGATCTGATGAGGATGCTGCTACTTATATTAACCTCATGGGGGAAGT 684
 532 GCAAGAGACATTTGTTAAGGTTAGCGGTGCTATTTGATCCCTCAGCTGGGAAATTT 591
 685 TGGCTTTCAGTACTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 744
 592 TGGCTAAGGACCTAACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 651
 745 TGGCTCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 804
 652 TGGTACTTCCATATTCAGTCCCATGATCCGGGGAAGTGGTGGTTCATCTAGAGT 711
 805 GTCATTTGGCCATGCTCCATTAATGAGCAAGAGTTGTTGTCATCTCAGCAACA 864
 712 GTTACATTTCCGTCAGTTACCTGTCATTTGCAATTTTCTGCCCAATGATCTCTT 771
 865 GTATATCTTTGAGAAAGAGCTTTATACATGATGATGATGATGATGATGATGATGATGAT 924
 772 CTGGAAGAACTGAGAAATGAAATTTTACATAACCGTTTGACAAATTAATCTCCAG 831
 925 GCTGCATTTGTTGTCAGAAAGAGATTTGATCTATCTCACCACCTTGACAGATAT 984
 832 AACAGAAATACCGTATGAGAGTACCTATATACCCCATTTACTTGAATAT 891
 985 CTTTGGGATCTCTACAAAGTTCTTGAGCTTATTCATGATGATGATGATGATGATGATGAT 1044
 892 GCGAACAGCTTGTATTTTACAAAAATACCTAAGAAACCGGTTATTAATCTCTTA 951
 1045 TTGAGGAAAGAGCTATTTCTGATTTGAGATATATATTAAGAGATGAAATCT 1104
 952 TCCAGAAAGAGGTTTAT-----GATCTAATCAAAACGAGATACAGAAATCT 999
 1105 CGATATATTTGATAGGCTCTGTAATAATAGTGTAAATAGCTTTGCTGTTGGGTGAA 1164
 1000 GATTCCTTGTATGACAGCTGTAAACAGGCTTTTGGGACCTTGACCTTATTA 1059
 1165 GATC---CAATTTGAGGCTTCAAGTTGATCTTCCAGAGATTTATGATTAATG 1221
 1060 GAAAGGATGACCTCGAAAGCGTTCCAGCGTCTCCATATATAGGTTCAAGAGATCAATGTTTC 1119

1222 ATTGCAAGATGCGATAAAATGCAAGGCTACATGAAAGTCAATATGAGACATGCT 1281
 1120 CATGGTCCACAGGGTATGACCATATATGGAACAAATGGGTGACAACTGGGATTTGGCG 1179
 1282 TTGCTGTCAGAGATTTATGATCTTAACTCATTTGAAGATTTGGTCCACATTAAGA 1341
 1180 TTGTCATTAATCTTTTTCGTCGAGGCTTCGCAAAAGACCTGAATTTCTAATAACA 1239
 1342 AAAGCTATACCTTATTAAGAAATTCACAGTTTAAAGATTTGACAGGATCTTAAT 1401
 1240 ATTGCTCTGCTATTAATCTTGTCTCATGCTCAATTTGACACCGAGTGGTTCAGGT 1239
 1402 AAATGTACCGTCACTTCAAAAGGTGCTTGGCTTTTCACTGAGATCATGATG 1461
 1300 A---GTTATAGGATTAAGAAAGGGGCTTGGGCTTTCACAAAAACAGAGGCTAT 1356
 1462 CCAATTTCTGACTGCAAGCTGAAAGGCTGAAAGCTGTTCTATTAATCAAAATTTGCA 1521
 1357 ACAGTGGCAATGTCAGTGCAGAAAGCAATTAAGCCATCATCATGAGTGAATACTTCC 1416
 1522 CCAGAAA---TAGTGTGAGCCATATGACGTGAAAGGATTAATGATTTCTGTAATGTC 1578
 1417 GTCCTTGTAGAGTACCATATGATTAAGAGTAAAGCTTTATTTGAAGCATTTGATG 1416
 1579 ATTCTCTACTACAGAA-----TGAAGATGGTGGTTTTCACATATGAGCTT 1626
 1477 TTATTTAAGCTACAAACCATCGATCTTTGATATATGATGCTTCTTTCACCTATGAAAA 1536
 1627 AAAGATCTTATTAATTTGTTGAGATATCAATCTCTGAAACTTTTGGTGAATGTT 1686
 1537 ATCAAGGCCCCCATGAGCAATGAAACCTTGAATCTCTGAAAGTTTGGTGAATATG 1596
 1687 ATTGATATCTTTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1746
 1597 GTAGATATCCATACGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1656
 1747 AAATTAATCTCTGGGATGCGCGAGAAAGAAATACACATTTGATGATTAAGCCATACC 1806
 1657 AA---GATCTCGCATTAAGAAAGAAATATGTCACGATCAGAAATGCGCATGAA 1713
 1807 TTCAATGAAAAATACAAAGCTTCAGATGATCATGATGATGATGATGATGATGATGATGAT 1866
 1714 TTCAATGAAAAATCTCAATTAACAGATGAAAGTTGATGAAAGCTGGGATATTTGTTTT 1773
 1867 ACTTACGCTGCTGTTTGGGGTAAAGGTCTGATTTGCTGTCGAGAAAGTTTCAGTAAT 1926
 1774 ACATATGCCGTATGTTTGTGATGAGGATTAACACCGTGGGGAGACCTATAGAAAT 1833
 1927 TGCTCAAGCATCCGTAAGCTTGTGAATTTCTGCTGCAAGCAGCTTCTCTGTGGC 1986
 1934 TCTCAACGGTAAGAAAGGTGGCATCTTGTGTCAGTAACAGATGAAGATGGCGGT 1893
 1987 TGGGAGAGAGTATCTGTCTCTGCAAAAGGTGATTAATCTGGAAGGCAACAG 2046
 1894 TGGGGGAAATCAATGAAGTCCAGTGA-----TTACATGTTATGATGATGATGATGATGAT 1947
 2047 TCTCATGTCGCAACATCGGGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2106
 1948 TGGTATGCTTCAACCGCATGAGGCTTAATGCACTTTTTCGCTGAATATCTTAAT 2007
 2107 AGAATTTGCAACCATGCAACCGGCGAGCTGATCTGATTAATTTCCAAATTTGAGAGAC 2166
 2008 AAAG-----AGTCATGACCGCGGATTTGACCTTTTAAATTAAGCAAGAAATGCC 2061
 2167 GGTGACTTTCCGACAGCAAGAAATTAAGGAGTCTTCAACAAAGATTTGATGATCACTAC 2226
 2062 GGGGAATGAAATTTGAAAGGTGAGAGGTGTTTCAACCACTTGTGCAATTTGAATAC 2121
 2227 GCGCATACAGAAACATATTTCCCATTTGGCGTGGGAGAAATAC 2271
 2122 CCAAGTATGATCTTATTTCCATTAAGGCAATTAAGTATGATC 2166

RESULT 8 US-09-248-796A-3811

Sequence 3811, Application US/09248796A
Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

PRIOR FILING DATE: 1998-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 3811

LENGTH: 747

TYPE: DNA

ORGANISM: Candida albicans

US-09-248-796A-3811

Query Match 2.9%; Score 74.4; DB 3; Length 747;
Best Local Similarity 51.6%; Pred. No. 7e-12;

Matches 199; Conservative 0; Mismatches 181; Indels 6; Gaps 1;

QY 505 GATGTTGGTGGGTTTGCATATTGAAAGTCAGACCATGTTGGCTCTGTCTTGAAT 564

DB 121 GATGTTGGTGGGTTTGCATATTGAAAGTCAGACCATGTTGGCTCTGTCTTGAAT 180

QY 565 TATATTACTCTGATGATTGCTAGGAGGAGGCTTAATGATGACAGAGGAGATGAGAA 624

DB 181 TATGATGCTCGGTTATTAAGAAATG-----AAAGATCATCATTTGGTTGTTAAG 234

QY 625 GCACGATGATGTTCTAGGAGCATGTTGCTACTTATTAACGTCATGAGGAGGAGAG 684

DB 235 GCAGAGAAACATTAATCATCTTTGGGTTGTCATTAAGATCAATGAGGTTAAGGCT 294

QY 685 TGGCTTTCACTGATCTGAGAGTATGATGATGTTGTAATATCCCTGCCCCCTGAGATA 744

DB 295 TGGCTTCTATTGTTGATTTATATGATGAGGAGGTTGTAACCACTCCACAGAACTT 354

QY 745 TGGCTCTCTTCATCATGCTCTTCATTCATCCAGAAAGATGTTGTTCTGCTCCGAGAG 804

DB 355 TGAAGATTACCGTACTGTTACCAATTCATCCAGCAATGAGGAGTACTACTAGGAGCT 414

QY 805 GTCTATTGTCGATGCTCTTATATGAGCAAGAGTTTGTGTCATCTCAGCAACA 864

DB 415 ATCTATTGTCGATGCTCTTATATGAGCAAGAGTTTGTGTCATCTCAGCAACA 474

QY 865 GTATTATCTTTGAGAAAGAGCTTTA 890

DB 475 TTTAAAGATCGAATTAATTA 500

RESULT 9 US-09-533-559-4882

Sequence 4882, Application US/09533559

Patent No. 6902887

GENERAL INFORMATION:

APPLICANT: Randy M. Berka

APPLICANT: Michael W. Rey

APPLICANT: Jeffrey R. Shuster

APPLICANT: Sakari Kauppinen

APPLICANT: Ib Groth Clausen

TITLE OF INVENTION: Methods For Monitoring Multiple Gene

FILE REFERENCE: 5849.200-US

CURRENT APPLICATION NUMBER: US/09/533,559

PRIOR FILING DATE: 2000-03-22

EARLIER APPLICATION NUMBER: 09/273,623

EARLIER FILING DATE: 1999-03-22

NUMBER OF SEQ ID NOS: 7860

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 4882

LENGTH: 652

TYPE: DNA

ORGANISM: Aspergillus oryzae

US-09-533-559-4882

Query Match 2.8%; Score 72.2; DB 3; Length 652;
Best Local Similarity 53.7%; Pred. No. 3e-11;

Matches 196; Conservative 0; Mismatches 163; Indels 6; Gaps 2;

QY 1393 GATCTTAATTAATGTTACCGTCAATTTCAAAAGGTTGCTTTTCACTGAGAT 1452

DB 55 GATCAGAGAAATGCTTACCGTCAATTTCAAAAGGTTGCTTTTCACTGAGAT 114

QY 1453 CATGATGAGCCAAATTTCTGATGCTCAAGCTGAGAGGAGTGAAGCTGTTCTATTATTC 1512

DB 115 CAGGCTTATGAGTATGAGGAGTCAAGCCAGGAGGCTTACGTTCAAGCATTCAGCTTCA 173

QY 1513 AAAATTGACCAAGAAATGTTGTTGATGAGCAGATGAGAGGAGTATGATTTCTGTA 1572

DB 174 AGAGATGACCAACTA-----TCTTAAGTATGATGACAGAGGCTTAAAGATGTT 228

QY 1573 AATGCTATTCTCTCACTACAGAAATGAGATGTTGTTTGAACAATGAGCTTAAAGCA 1632

DB 228 GACTCTGCTGCTCATGCAAAATCTTCTGAGGTTTACAGATGAGCCAGCT 288

QY 1633 TCTTAATTAATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGAT 1692

DB 289 GGTGAGCCAGATGAGTATGATGATGATGATGATGATGATGATGATGATGAT 348

QY 1693 TATCTTATGTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1752

DB 349 TACGATATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 408

QY 1753 TATCC 1757

DB 409 TATCC 413

RESULT 10

US-08-998-416-229/C

Sequence 229, Application US/08998416

Patent No. 6239264

GENERAL INFORMATION:

APPLICANT: Philippen, Peter

APPLICANT: Steiner, Sabine

APPLICANT: Mohr, Christine

APPLICANT: Wendland, Jurgen

APPLICANT: Knechtel, Philipp

APPLICANT: Redischung, Corinne

TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPYII

TITLE OF INVENTION: AND USES THEREOF

NUMBER OF SEQUENCES: 1152

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6239264artis Corporation

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: No. 6239264ch Carolina

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/998,416

FILING DATE: 24-DEC-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:


```
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 229:
SEQUENCE CHARACTERISTICS:
LENGTH: 539 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1211RP
US-08-998-416-229
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Query Match 2.8%; Score 70.4; DB 3; Length 539;
Best Local Similarity 57.1%; Pred. No. 9,6e-11;
Matches 128; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

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QY 604 GCACAGGGGAAATGAGAGAGGACGCTGACTGATTTAGAGGATGCTGCTACTTAT 663
DB 273 GAACACATGCTGATCAGCGGGGCGGAAGACCTGCTGCGCATGGGGGCTCTATTGGC 214
QY 664 ATACGTCATGGGGGAGATGCGCTTTCAGTACTTGAAGTGTATGAATGCTCGGAAT 723
DB 213 TCGCCGTCAGGGGCTAAAGTGTGCGCTTCCGCTCAATTATACAGTGGGAGGCGCTG 154
QY 724 ATCCCGTCCCGCTGAGATATGGTCCCTTCATCATGCTTCCATTTATCCAGGAAG 783
DB 153 AACCCAGGCGCACAGAGATATGCGTCCGCTACAGTTTCTTATCACCCGCTCGC 94
QY 784 ATGTGTGTCTACTGCGGATGCTTATTTGCCGATGCTCTACTT 827
DB 93 TGTGTGGTACATACGCGTGTCTATCTTTTGGCGATGAGTACTCT 50
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RESULT 11
US-09-313-294A-804
Sequence 804, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PI-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
PRIORITY FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 804
LENGTH: 173
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
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OTHER INFORMATION: Inocyte ID No. 6476212 700549863H1
US-09-313-294A-804
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Query Match 2.3%; Score 58.2; DB 3; Length 173;
Best Local Similarity 63.0%; Pred. No. 2,6e-07;
Matches 109; Conservative 0; Mismatches 58; Indels 6; Gaps 1;

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QY 1485 AGGACTGAAGCTGTTCTATTACTATCCAAATTGCACACAGAAA-----TAGTTGTGGA 1538
DB 1 AGCAGCTTAAGGCTGACTGTGTCTGCTCAAGATCTCAAAACAAAACAACTTTGTGGGGA 60
QY 1539 GCCAATAGACGTGAAGCATTTATGATTTCTGTAAATGATCAATTTCTCAGTACAGAAATGA 1598
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DB 61 TCCAATAGAAAGAGAAAGGTTGCATGACGCTATGATTCCTTCTATCTTTGGCAAA 120
QY 1599 AGATGCTGTTTCCACATATGAGCTTAAACGATCTTATATATGTTGAGAGA 1651
DB 121 AGATGGACCTTTTCTACATATAGTGCAAAAGAACTTATCTTGTGTTAGAGA 173
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RESULT 12
US-10-104-047-1011
Sequence 1011, Application US/10104047
Patent No. 6943241
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241el full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
PRIORITY FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1011
LENGTH: 3600
TYPE: DNA
ORGANISM: Homo sapiens
US-10-104-047-1011
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Query Match 1.8%; Score 47.2; DB 3; Length 3600;
Best Local Similarity 67.0%; Pred. No. 0.0038;
Matches 67; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

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QY 2165 ACGGTGCTTTCCGACAGAGAAATATGAGAGCTTCAACAAGATTCATGATGTCAT 2224
DB 1480 ATGGGAGCTGGCGCAGAAAACATGCTGCGGCTTCAACAGTCTTGCGCATCTCT 1539
QY 2225 ACGCGCATACAGAAACATATTCCTCCATTTGGCGGTGGG 2264
DB 1540 ACACGAGCTACAGAGACATCTTCCCATCTGGGCCCTCGG 1579
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RESULT 13
US-09-806-708B-22/c
Sequence 22, Application US/09806708B
Patent No. 6784342
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
PRIORITY FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIORITY FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 1141
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: promoter
LOCATION: (1)-(1141)
OTHER INFORMATION: consensus sequence of A.T., L.A., and B.N. PAB1 promoters
US-09-806-708B-22
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Query Match 1.8%; Score 46; DB 3; Length 1141;
Best Local Similarity 11.5%; Pred. No. 0.0044;
Matches 95; Conservative 310; Mismatches 410; Indels 10; Gaps 4;

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DB 980 WAGNNMRYGAAAGNKGWCAAMATWGBWADTAKGKNNNNNNNTTVDVRRMAMKAKNNN 921
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US-08-916-421B-1
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Query Match 1.7%; Score 44; DB 3; Length 1664976;
Best Local Similarity 46.9%; Pred. No. 1.5;
Matches 137; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

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Db 1268220 TAAATCTATAAAACCTTAGTCAATAGTTCATGCCACAGAGATGAGATTAAGGTTTAG 1268161
Qy 1178 AGGCTTCAAGTTCATCTCCAGATTTATGATTAATGATTCAGAAAGATGCA 1237
Db 1268160 AGCGATGAGATTTTATTTTCTGAGAACGTTGATGAGAAAAATGACTTAATGATGTG 1268101
Qy 1238 TGAATGACAGGCTCAATGAAAGTCACTATGAGACACTGCTTTGCTCCAGCAA 1297
Db 1268100 TTGAAACGACGAGATATTTTGAAACCCATTAATAATTCATATGTCATATGTAAGGA 1268041
Qy 1298 TTAATGATCTAATCCTGATTAAGAAATTTGCTCCAACTATPAAGAAAGCTATACCTATA 1357
Db 1268040 AAGAGCTAAGAAAGATATTTAAACATATTTAGTATTAATPAATCAGATGATTAATA 1267981
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Db 1267980 TAAATTAACGTAAGAAAGATTTACACTTAAGAGTTGAGATTAACAAATTTTA 1267929
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RESULT 15

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US-09-692-570-1/c
Sequence 1, Application US/09692570
Patent No. 6797466
GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
Patent No. 6797466
FILE REFERENCE: PB275C1
CURRENT APPLICATION NUMBER: US/09/692,570
CURRENT FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
PRIOR APPLICATION NUMBER: US 08/916,421
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
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Query Match 1.7%; Score 44; DB 3; Length 1664976;

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Matches 137; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

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